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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                              αααα
                                                                                                                    ααα
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92:
                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                  Score
                                                                                                                                                                                                            18
         seq length: 0 seq length: 2000000000
                                                                                                                                                                                                            derived by analysis of the total score distribution.
                                                                                                                                                                Query
Match Length DB
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564
99.7 10777
98.0 150110
98.0 150214
7.8 125020
7.6 125020
7.1 194533
7.1 320658
7.1 130344
7.1 1103034
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7.1 111934
7.1 114936
6.9 184532
6.9 215604
6.8 110000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      March 25, 2006, 16:11:03 ; Search time 3009.5 Seconds (without alignments)
10652.835 Million cell updates/sec
                                                                                                                                                                                                                                               5883141 seqs, 28421725653 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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gb_pat:
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AC163209
AC111047
        AC124345
AC021667
AC160979
                                                                                                                                                HS11Q13RP
                                                                                                                                                                 ij
                                                            AC067978
                                                                                                                                                                                           SUMMARIES
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Biocceleration Ltd.
                                                                 AP006345 Homo sapi
AF429315 Homo sapi
AF429315 Homo sapi
AC093592 Homo sapi
AC073344 Homo sapi
AC073344 Homo sapi
AC0145527 Atelerix
AC163209 Mus muscu
                                                                                                                                                Y12377 H.sapiens F
                                                                                                                                                                Description
                                                                                                                                        AC097722 Homo sap:
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RESULT 1
HS11Q13RP
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

H.sapiens FGF/int-2 gene upstream flanking Y12377

region. linear

PRI 02-MAR-2000

10777 bp

Homo sapiens (human)

Alu repeat; FGF-3 Y12377.1 GI:1934871

gene; int-2 gene; L1 repeat; MIR repeat.

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37	37	37	37	37.2	37.2	37.2	37.4	37.4	37.4	37.4	37.4	37.4	37.6	37.8	37.8	37.8	38	38	38	38	38	38	38.2	38.2	38.2	38.2
6.6	6.6	6.6		6.6	6.6	6.6	6.6	6.6		6.6	6.6	6.6	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.8	6.8	6.8	6.8
157585	2500	1785	1422	294817	36628	21670	240039	223357	213590	207735	187911	184866	114694	138129	134362	111370	205854	190018	142979	121103	119613	110000	178778	74871	2777	2777
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BX322664	SSU65940	HSTPRMPL3	BT020874	AC114626.	AF037222	AF508041	AC111926	AC111958	AC154101	AC130279	AC136867	AL611934	AL355500	HS102D24	AC084853	AC067815	AC138186	AC148588	AC000029	AP006623	AC138582	LMFLCHR26_2	AC132936	AC137095	AK095212	AX833454
BX322664 Zebrafish	U65940 Streptomyce	U68161 Human throm	BT020874 Bos tauru	AC114626 Mus muscu	AF037222 Human DNA	AF508041 Homo sapi	AC111926 Rattus no	AC111958 Rattus no	AC154101 Mus muscu	AC130279 Mus muscu	AC136867 Rattus no	AL611934 Mouse DNA	AL355500 Human DNA	AL021391 Human DNA	AC084853 Homo sapi	AC067815 Homo sapi	AC138186 Homo sapi	AC148588 Pan trogl	AC000029 Homo sapi	AP006623 Homo sapi	AC138582 Pan trogl	Continuation (3 of	AC132936 Homo sapi	AC137095 Homo sapi	AK095212 Homo sapi	AX833454 Sequence

#### ALIGNMENTS

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AC067978 Homo sapi
AF281074 Homo sapi
AC007362 Homo sapi
AC159874 Bos tauru
AC124345 Mus muscu
AC160979 Mus muscu
AC160979 Mus muscu
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                       repeat_region
                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                     Brison,O.

Direct Submission

Submitted (04-APR-1997) O. Brison, Lab. de Genetique Oncologique,
Submitted (04-APR-1997) O. Brison, Lab. de Genetique Oncologique,
CNRSURA1967, Institut Gustave-Roussy, 39 Rue Camille Desmoulins,
94805 Villejuif CEDEX, FRANCE
The BamHI site at the 3' end of this sequence (nt 10772)

corresponds to the BamHI site at the 5' end of the FGF-3/int-2 gene
sequence (nt 1; X14445), as ascertained by sequencing through this
site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Djenabi,S., Brison,O., Galdemard,C. and Lavialle,C.
Sequence analysis of the transcription control region upstream of the human FGF-3 gene
DNA Seq. 10 (4-5), 317-329 (1999)
                                                                                                                                                                                                                                                                                                      Related sequence: B04369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.
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                            /germline
489. .631
                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                            /tissue_type="placenta"
/clone_lib="lambda D3, Clontech cat#HL1067J lot 1221"
                                                                                                                             map="q13"
                                                                                                                                                  chromosome="11"
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  rpt_family="MIR2"
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ACCESSION
VERSION
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                                                            150110 bp DNA linear HTK
Homo sapiens chromosome UNK clone RP11-186D19, WORKING
SEQUENCE, 9 unordered pieces.
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AC097722.2 GI:18308824
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                   AGGCAGTGGCGTCTTTCGGACTTC
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                                                                                                                                                                                                      AGCACTGCCCGCCGCCTCTGCGATGCAGTCCTCCTGGCCACCTGAGAACAGCCTGTAGAG
                                                                                                                                                                                                                    AGCACTGCCCGCCGCCTCTGCGATGCAGTCCTCCTGGCCACCTGAGAACAGCCTGTAGAG
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7715: .7844
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2605. .2752
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7417. .7568
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7003. .7242
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3224. .3514
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                                                                            HTG 24-JAN-2002
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AUTHORS
TITLE
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                                    misc_feature
                                                                                                                 source
                                                                                                                                                   9899
14020
14120
19393
19493
19493
24873
24873
24873
68993
68993
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4045
9799
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Sequencing vector: M13; 54*
Sequencing vector: M13; 54*
Sequencing vector: Plasmid; 46*
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.99019
Consensus quality: 147449 bases at least Q30
Consensus quality: 148263 bases at least Q30
Consensus quality: 148688 bases at least Q20
Insert size: 150429; sum-of-contigs
Quality coverage: 8.73 in Q20 bases; sgarose-fp
Quality coverage: 7.35 in Q20 bases; sgarose-fp
Quality coverage: 7.35 in Q20 bases; sgarose-fp
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Submitted (22-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jan 24, 2002 this sequence version replaced gi:16306472.
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1 (bases 1 to 150110)

Waterston, R. H.

The sequence of Homo sapiens
Unpublished
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number be preserved.
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/chromosome="UNK"
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estimated_length=unknown
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                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                       14119: gap of unknown length
1939: contig of 5273 bp in length
19492: gap of unknown length
24872: contig of 5380 bp in length
24972: gap of unknown length
44972: gap of unknown length
43958: contig of 18986 bp in length
44058: gap of unknown length
68992: contig of 24934 bp in length
68992: gap of unknown length
104669: contig of 35577 bp in length
104769: gap of unknown length
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104769: gap of unknown length
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4044: gap of unknown length
9798: contig of 5754 bp in length
8898: gap of unknown length
14019: contig of 4121 bp in length
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clone_end:SP6
vector_side:right"
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/note="assembly_name:Contig26"
9799. .9898
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24873. .24972
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19493. .24872
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9899. .14019
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24973. .43958
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14120. .19392
!note="assembly_name:Contig28"
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14020. .14119
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Pred. No. 1.7e-121;
0; Mismatches 0;
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Totoki,Y. and Sakaki,Y.
Homo sapiens genomic DNA
Published Only in Database (2003)
2 (bases 1 to 150214)
Hattori,M., Toyoda,A., Taylor,T.D., K.
Totoki,Y. and Sakaki,Y.
Direct Submission
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AP006345
AP006345.4
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On Aug 5, 2005 this sequence version replaced gi:48290861.
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Mammalia; Eutheria;
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Homo sapiens
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ACAGGGTCCCATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAA
                      ACAGGGTCCCATCCACGTACCAGCCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAA
                                                                                                                                              GGGGTCTTGCCATGGTGGGCACAGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCC
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/clone="RP11-186D19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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genomic DNA, chromosome
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Pred. No. 1.7e-121;
0; Mismatches 0;
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11 clone:RP11-186D19, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (05-OCT-2001) Psychiatry, Johns |
Institutions, 600 N. Wolfe St., Baltimore,
Location/Qualifiers
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1 (bases 1 to 125020)

Holmes, S.E., O'Hearn, E.,
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AF429315
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                               /map="16q24.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
                   /trānslation="MSSGGRFNFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
HGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
NGAKYEGTWSNGLQDGYGTETYSDG"
                                                                                                                                                                                                      /product="junctophilin 3"
complement(<36507. .36887)
                                                                                                                                                                                                                                                                                                                                                                              complement (35581. .35746)
                                                                                                                                                membrane and endoplasmic reticulum"
                                                                                                                                                                                                                                                               complement (<36507. .>36887)
                                                                                                                                                                                                                                                                                                                                         _12,
12,15
                                                                        /product="junctophilin 3"
/protein_id="AAL40941.1"
/db_xref="GI:17646245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                            codon_start=1
                                                                                                                                                                   note="component of the junctional complex between
                                                                                                                                                                                       gene="JPH3"
                                                                                                                                                                                                                                             gene="JPH3"
                                                                                                                                                                                                                                                                                  'note="synonym: JP3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/chromosome="16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ingersoll-Ashworth, R.G., Ross, C.A. and Margolis, R.L.
                                                                                                                                                                                                                                                                                                                     lement (<36507. .>36887)
                                                                                                                                                                                                                                                                                                                                       unit="ctg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                              type=tandem
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lin 3 (JРНЗ)
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timore, MD 21287, USA
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                                                                                                                                                                     plasma
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Best Local Similarity
                                                                                                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens junctophilin 3 (JPH3)
AF429315
                                                                                                                                                                                                                       1 (bases 1 to 125020)
Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H Holmes,S.E., O'Hearn,E., Fleisher,A., Stevanin,G., Brice,A., Potter,N.T., Ross,C.A. and Margolis,R.L.
A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2
Nat. Genet. 29 (4), 377-378 (2001)
                                                                                                    Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
                                                                                                                                            Holmes, S.E., Ingersoll-Ashworth, R.G., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                            11694876
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                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSMSSKGWRGYAGRGCYSSSMWSTRKRRSKCYSYKSYKKGRGKMKGWGGMKRGSKYWSSM 17302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKKKĠĊTGYRGMSSKKSGYKSMRGMRGSSYSTSCWKSCWGYSWMKCMKYMSYKKKRRSMR 17362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCCCTGGTGCCAGCCTCTGGAAGTC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGSTGRSMKKKKGYSKYSRGMKGKKKTCYCMWKYYKYRKTSMCWWYYMKSWGYKRYKRCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRKGRKCMSSRKMKMYKSYYRRKRWMTCMKMCYSMYMAMYCRSMCCMCMCKSCCGCYSMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGRMSSKSCYRSGTRRRCMKSKCRRGSRGKSMGMTRGRSGGKTSYSAKGSGRGCYYCWGW 1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGGTGGGGCTGGGCTGGGCCAAGGCCA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RMGKTGCNYMYRRSRAMMNGNAAAAGCTTCCCCCANTNGGGGGGAAAAAGGGGCGSASRASCY 17182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCCAGGTGGCTGCAGAAGGT--CCCTCGCAGTCATGAAACCAAGGGAAGCCTTGGGAAAC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKMKRSSWSKCYSTKSYKSGRRKSKGWGRSTKSKAKSSWRMAGSKCTYGSSYWSNNRRNN 17242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCACACTCACTGCCTTTGCAGGGTTGGGGCTTCCAGTCACAGGGTCCCATCCACGTACCA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGGCAGGGCCAGGGCAGCCGTCAGGTGGGTGACGGCAGGGGTCTTGCCATGGTGGGCAC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGATGCAGTCCTCCTGGCCACCTGAGAACAGCCTGTAGAGAGGCAGTGGCGT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCCAGCACTGCCCGCCGCCTCTG 500
                                                                                                                                                                                     (bases 1 to 125020)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 222;
organism="Homo sapiens"
                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:17646244
  _type="genomic DN
xref="taxon:9606"
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Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene, partial cds.
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                                                                                                                                                                  Ross, C.A. and Margolis, R.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 125020;
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                                                                                                                                                                                                                                                                                                                               Hwang, H.S.,
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Best Local Similarity 11.5%;
                                                                                                                                 ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                      52106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51746 KSAYSCMYMSKACKSSYCAKRSGCYKKYWGSMYYSTGSRSMWYTSTYSYCMYMSMMWSY 51805
                                                                                                                                                                                                                                                                                                                                                                                                                                                           52046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51986 RYRWRKMCWGMWTRKSKĠKSYSNSSWGWMWGKGTSYMCCASSYAMSCRKGMRSATSWGCC 52045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332
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                                                                                                                                                                          AC093592
AC093592.3
HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 GCACACTCACGGTGACTCACCCCCATGTGGCTGGAGGCGAGGGGAGCCTCCTGAGGCAGGG 91
1 (bases 1 to 184533)
Meyer,R., Doebber,A. and Bielicki,L.
The sequence of Homo sapiens BAC clone
                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                    Homo sapiens BAC clone RP11-50L21 from 4,
                                                              Hominidae; Homo.
                                                                                                                                                                                                                                                             AC093592
                                                                                                                                                                                                                                                                                                                                                                                                              GGCATGGCTTTGATTTAGTGAGAGGGTGGG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CMMRSYTTSCTCYYGCYCMWKGKYWKRRSSYKSCYKKKSMTKYSMRGMSCYRGSRYMYSY 51985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRSCCMSWKTGYCKGKKSWSMKCATTGMKSCARKSMSCYCGKMCRRASCWGCYKCMSMKT 51925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGGGCAGCCGTCAGGTGGCTGACGGCAGGGGTCTTGCCATGGTGGCACAGGGGCTGC 151
                                                                                                                                                                                                                                                                                                                                                                      RGSMGKGSMTKKSKGTGKGMWGRGGSWGKS 52135
                                                                                                                                                                                                                                                                                                                                                                                                                                                           YMSYRSASWCWGSTGSMRSYKSTWRSCWSCMRGSMSYYSRMRGKGGCASWSCYRKKSKRK 52105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGCAGAAGGTCCCTCGCAGTCATGAAACCAAGGGAGGCTTGGGAAACCACATCTGAAG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAATGTTTCCCATTAAGGAAAGTGTGTGGCCGGCCATGCCCCCCAACGTTGCACACTCA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATACAGCTTACTCAGTGACAATCGAGTCCCTGGTGCCAGCCTCTGGAAGTCTGGAAGTGA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCCTTTGCAGGGTTGGGGGCTTCCAGTCACAGGGTCCCATCCACGTACCAGGCCCAGGTG
                                                                                                                                                   sapiens (human)
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complement (<36507. .>36887)

/gene="JPH3"

/note="symonym: JP3"

/note="symonym: JP3"

complement (<36507. .>36887)
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/note="isolated from a patient with Huntington's D1sease-Like 2 (HDL2)"
complement (35581. .35746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="junctophilin 3"
/protein id="AAL40941.1"
/db xref="GI:17646245"
/translation="MSSGGREWFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
/translation="MSSGGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="component of the junctional complex between membrane and endoplasmic reticulum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="junctophilin 3"
complement(<36507. .36887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGAKYEGTWSNGLQDGYGTETYSDG"
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                                                                               Direct Submission
Submitted (13-MAY-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (03-DAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (07-NOV-2001) Genome
University School of Medicine,
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                                                                                                                                                                                           Wilson, R.K.
                                                                                                                                                                                                            University, 4444 Forest (bases 1 to 184533)
                                                                                                                                                                                                                                            Submitted (09-JAN-2002)
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             Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0050L21
                                                              Center: Washington University Center code: WUGSC
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t Park Parkway, St.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

### MAPPING INFORMATION:

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Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, se http://genome.wustl.edu sequence, see

### SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org pBACe3.6

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is this clone is at base position 1 of base position 184533 of RP11-50L21. RP11-628B17. Actual RP11-50L21; actual Actual start ctual end is a at of

AC073344 and AC016032 was used to finish thi Polymorphisms have been identified between finish this clone AC073344 and

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Homo sapiens BAC clone RP11-628B17
AC073344
AC073344.7 GI:19848493
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                                                       Harris, A., Meyer, R. and Nguyen, C.
The sequence of Homo sapiens BAC
Unpublished (2001)
                                                                                                                                                                       1 (bases 1 to 192573)
Sulston, J.E. and Waterston, R.
                                                                                                                                                                                                                                                  Homo sapiens (human)
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Submitted (14-JUN-2000) Genome Sequencing Center, Washington
                                                                                                                                      Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                             3 (bases 1 to 192573)
Waterston,R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="CpG_island (%GC=74.2, o/e=0.97, 59958. .61269 /note="CpG_island (%GC=76.4, o/e=0.85, 72793. .73003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Homo sapiens KIAA1430 protein, mRNA (cDNA clone MGC:40366 IMAGE:5240222), complete cds.; H_NH0050L21.1 This gene was based on gi(20988136) Continued from H_NH0628B17.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-11"
complement(19506..26531)
/gene="KIAA1430"
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elsrqaekpgskstiprsadhppklyhsalnrqkeqqrierenltislchpgwsavt"
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/mol type="genomic DNA"
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/db_xref="GI:63992942"
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                                                                                                   University, 4444 Forest rark Avenue, v. ______ gi:18677646 on Mar 30, 2002 this sequence version replaced gi:18677646 on Mar 30, 2002 this sequence center
                                                                                                                                    Direct Submission
Submitted (16-APR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6
                                                                                                                                                                                                                                                      Direct Submission
Submitted (30-MAR-2002) Genome
University School of Medicine,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (15-FFB-2002) Genome Sequencing Center, Washing
University School of Medicine, 4444 Forest Park Parkway,
MO 63108, USA
                                                                                                                                                                                                                   Waterston, R.
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                Center: Washington University Genome Sequencing Center code: WUGSC
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: saplens@watson.wustl.edu
Contact: Summary Statistics
Center project name: H_NH0628B17
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COMMENT

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise noted:

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

### SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org pBACe3.6 Frengen, E.,

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-714G18. this clone is at base position 1 of RP11-628B17; base position 192573 of RP11-628B17. Actual start actual end is at

Polymorphisms exist between AC073344 and AC093592. Data from AC093592 was used to finish AC073344. /mol\_type="genomic\_DN /db\_xref="taxon:9606" /chromosome="2" organism="Homo sapiens" Location/Qualifiers . .192573

clone="RP11-628B17"

FEATURES

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repeat_region
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5136. _soan
                                                                   /note="match to EST 6791. .7081
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381. .445
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3330. .3634
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/note="similar to Homo sapiens EST BP172452
(NID:g13338666)"
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(NID:g16485359)"
1466. .1811
                                              rpt_family="Alu"
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255. .1811
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| Thote="match to EST BG616006 (NID:gl3667377)"
| 1079. .1331
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                                                                                                                                                  _family="tRNA-Gln-CAG"
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Submitted (19-JUL-2003) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA Draft Sequence Produced by Berkeley PGA Web site: http://pga.lbl.gov Center Code: PGABERK Center Project Name: E024-283G23
                                                                                             2 (bases 1 to 320658)
Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Peng, Z., Malinov, I. and Rubin, E.M.
Direct Submission
                                                                                                                                                                                Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Peng, Z., Malinov, I. and Rubin, E.M. Direct Submission
                                                                                                                                                                                                                                                                                                  AC145527.1 GI:32996788
HTG; HTGS PHASE1; HTGS DRAFT.
Atelerix albiventris (middle-African hedgehog)
Atelerix albiventris
                                                                                                                                                                                                                                                                                                                                                                                                    AC145527 320658 bp DNA Atelerix albiventris clone LB4-283G23,
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Insectivora; Erinaceidae;
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AC145527
                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                Erinaceinae; Atelerix.
1 (bases 1 to 320658)
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8027. .8317
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8381. .8759
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1943. .12383
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0957. .11251
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)690. .9986
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8760. .9071
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Pred. No. 27;
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* NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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These libraries are available through the BACPAC Resources Center:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.chori.org/bacpac/libraryres.htm as LBNL-1 to LBNL-4.
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                                                                             /organism="Atelerix albiventris"
/mol_type="genomic DNA"
/db_xref="taxon:9368"
                                                                                                                              1. .320658
estimated_length=unknown/
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1761. .4860
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46012: gap of unknown length
52370: contig of 6358 bp in length
64704: contig of 12234 bp in length
64804: gap of unknown length
76264: contig of 11460 bp in length
76264: contig of 11460 bp in length
94758: contig of 13934 bp in length
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118713: contig of 23855 bp in length
118813: gap of unknown length
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118921: contig of 29208 bp in length
148021: contig of 30818 bp in length
149039: contig of 30818 bp in length
179039: gap of unknown length
179039: gap of unknown length
179039: gap of unknown length
1211754: contig of 32715 bp in length
263200: contig of 32715 bp in length
263200: contig of 51346 bp in length
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2425: gap of unknown length
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7844: contig of 2984 bp in
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                                                                                                                                                                                    153129 bp DNA linear ROD 03-AUG-
Mus musculus chromosome 3, clone RP24-11708, complete sequence.
AC163209
AC163209.2 GI:71725541
                                             1 (bases 1 to 153129)
Birren,B., Nusbaum,C. ar
Mus musculus chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCAGCCCTGCCTCAGAAAACAGAAGGACGCAGCACACTCACGGTGACTCACCCCCATGTG
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
Sciurognathi; Muroldea; Muridae; Murinae; Mus.
                                                                                                                                           Mus musculus (house mouse)
 Birren, B., Nusbaum, C.,
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                               Unpublished
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                                                 and Lander,E.
me 3, clone RP24-11708
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Pred. No. 26;
 Lander, E., Abouelleil, A., Allen, N.,
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RRS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Changel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-pierre, N., Hafez, N., Bastien, J., Gardyna, S., Graham, L., Grand-pierre, N., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Machen, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Murphy, T., Naylor, J., Manon, J., Manning, J., Matthews, C., Murphy, T., Naylor, J., Manon, C., Murphy, T., Naylor, J., Manon, S., Subyback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stouban, K., Travers, M., Vassilev, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassilev, V., Venkataraman, V.S., Viel, R., Noto, R., Nather, N., and Zody, M., Direct, Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (03-AUG-2005) Broad Institute of MIT and Harvard, Charles Street, Cambridge, MA 02141, USA
Charles Street, Cambridge, MA 02141, USA
On Aug 3, 2005 this sequence version replaced gi:67003668.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                                                                                                                                                                                      Center clone name: 117_0_8
                                                                                                                                                                                                                                                                                                                                                          Center project name: L32928
                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
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2843. .2893
/rpt_family="AT_rich"
complement(2985. .3180)
                                                                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                              clone="RP24-11708"
clone_lib="RPCI-24 Male Mouse BAC"
                                                                                                                                                          chromosome="3"
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5441. .5470
/rpt_family="(GAA)n"
5748. .5876
                                /rpt_fami.
24051. .2
                                                                                                                                                                                           /rpt_family="L1 MM"
complement(23405..23879)
/rpt_family="MERVL_LTR"
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9937. .100ps
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/rpt_family="B3"
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/rpt family="MIR"
21915. .21942
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/rpt_family="L1MA4A"
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/rpt_family="L1"
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/rpt_family="B4"
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6984. .7110
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19454. .20704
          rpt_family="(TCTCC)n"
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                                                                                                                                                                                                                                                                                                      76120 GACAGGAGCCAGGGGTGGAGCTAGGGTAGGAGGCAGGGCGGGGCCAGAGCAGAAGGCAGG
                                                                                                                                                                                                                                                                            421
                                                                                                                                                                                                                                                                                                                                361
                                                                                                                                                                                                                                                                                                                                                                                  301 ACAGGGTCCCATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAA 360
                                    AC111047
230041 bp DNA linear ROD 10-OCT-2 Mus musculus chromosome 3, clone RP23-176H24, complete sequence. AC111047
AC111047.9 GI:37620322
HTG.
                        Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 3, clone RP23-176H24
                                                                                                                  Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="single clone coverage" 31116. .31151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (33166.
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complement(31417. ...
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5. .26707
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family="MIR"
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.307AE
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family="IAPEY LTR"
lement (29660 . .29993)
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Pred. No.
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                                                     source
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangel, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Gord, S., Goyette, W., Jiev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McEwan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Melmga, V., Murphy, T., Naylor, J., Nguyen, C., Micol, R., Norbu, C., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Norbu, C., Norman, C.H., O'Connor, T., O'Ononell, P., O'Nell, D., Oilver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rogetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Viel, R., Vo, A., Wilson, B., M., X., Wyman, D., Ye, W.J., Young, G., Jahoun, J., Zembek, L., Zimmer, A. and Zody, M. Vassiliev, H., Viel, R., Peterson, Whithhead Trational Joy, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boguslavkiy, L. Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., MacLean, C., MacClean, C., MacConald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., MacConald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Mendarim, J., Meneus, L., Mihova, T., Mlengs, V., Murphy T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Weil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, S., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Research, 320 Charles Street, Cambridge, MA 02141, USA On Oct 10, 2003 this sequence version replaced gi:34495134. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
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Birren,B., Nusbaum,C. and Lander,E.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-OCT-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                 Center project name: L19822
Center clone name: 176_H_24
                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
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                                                                                                                                                                                             Location/Qualifiers
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                                                                                              organism="Mus musculus"
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misc\_feature

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1. .21291
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Jd.
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15349.
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15203
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      .18891
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                                                                  .15975)
 REFERENCE
AUTHORS
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LOCUS
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Best Local Similarity 52.4%;
Matches 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 ACAGGGTCCCATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAA 360
                                                                                                                                                        103034 bp DNA linear HTG 03-JUL-2000 Homo sapiens chromosome 2 clone CTD-2350K7 map 2, WORKING DRAFT SEQUENCE, 15 unordered pieces.
1 (bases 1 to 103034)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 2, clone CTD-2350K7
                                                                                            AC067978.2 GI:8901271
HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                 Hominidae; Homo.
                                                                                                                                                                                                                                                                                      GGCGGGGCCAGGCAGGAGCCAGGGCAGGGCAGGCAGG 21471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 3, 2000 this sequence version replaced gi:7656720. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: L9518
Center clone name: 2350 K 7
Center clone reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 95545 bases at least Q40
Consensus quality: 95446 bases at least Q30
Consensus quality: 100858 bases at least Q20
Insert size: 98000; agarose-fp
Insert size: 101634; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
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/mol_type="genomic DNA"
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Rossignol,M., Gagnon,M.L. and Klagsbrun,M.
Direct Submission
Submitted (21-JUN-2000) Surgical Research, Children's Hospital,
Longwood Ave, Boston, MA 02115, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isoforms
Genomics 70 (2), 211-222 (2000)
11112349
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Rossignol, M., Gagnon, M.L. and Klagsbrun, M.
Gensmic organization of human neuropilin-1 and neuropilin-2 g
identification and distribution of splice variants and solubl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spliced.
AF281074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF281074.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF281074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCCTGCCTCAGAAAACAGAAGGACGCAGCACACTCACGGTGACTCACCCCCCATGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGATGAGAGGTGTTCCCCAAGGCCTGGGCCA 93077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCTCCCTCGGAAACCAGGAAGGCTGGGCACCCTCCGTGGGCCTCACCCTCATTTGGAA 93046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111934 bp DNA linear |
Bapiens neuropilin 2 (NRP2) gene, complete cds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71309. .71408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Join(<3518. .3590,17760. .17937,36403. .36584,42688. .42918,
43995. .44150,46123. .46292,48101. .48256,60728. .60872,
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83879. .84141,85679. .85775,86988. .87023,108610. .108660,
111118. .>111422)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.1%;
                                                                                                                                                                                                                                                                                     .>111422)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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Pred. No. 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 103034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRI 21-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                           for VEGF165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEGF165 and
                                                                                                                                               and
                                                                                                                                           semaphorins class3"
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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
AC007362/c
                                                                                                                                                                                                                                                                                                                                                                EYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                          ORGANISM
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1 (bases 1 to 116039)
Bemis,G., Kalicki,J., Maupin,R. and Davidson,T.
The sequence of Homo sapiens BAC clone RP11-150F11
                                                                                                                                                                                                                                                                                                                                                                    HTG.
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    AC007362
AC007362.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens BAC clone RP11-150F11 from 2,
                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC007362
                                                                                                                                                Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGATGAGAGGTGTTCCCCCAAGGCCTGGGCCA 66628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGGCGAGGGAGGCCTCCTGAGGCAGGGCCA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCTGCCTCAGAAAACAGAAGGACGCAGCACTCACGGTGACTCACCCCCCATGTGGCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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// COGOT_BLATE
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SASSTQEYLMSPSAARLVSSRSGMFPRIPQADGGEENLOVDLGTPKTVKGVIIQGARG
GDSITAVEARAFVRKFKVSYSLAGKDMSTIQDARTQDFKLTGQDKLFGNMHYDTFDIRRFDPI
PAQYYRVYBERWSPAGIGMRLEVLGCDWTDSKETTVETLGPTVKSEETTTFPYFTEEAT
ECGENCSFEDDKDLQLPSGFNCNFDFLEEPCGMMYDHAKMLRTTWASSSSPNDRTFPD
DRNFLRLQSDSQREGQYARLISFPVHLPRSFVCMSFQYGTGGRGVALQVVREASQES
KLLMVIREDQGGEWHGRIILDFSYDMSYGIVEGGVIGKGRSGTAIDDIRISTUVPLE
NCMEPISAFAGENFKGGTLLFGTEFTVDTVPMQPIPAYWYYVMAAGGAVLVLVSVALA
LVLHYHRFRYAAKKTDHSITYKTSHYTNGAPLAVEFTLTIKLEQDRGSHC"
join(13518. 3590, 17760. 17937, 36403. 13584, 42688. 42918,
43995. 44150, 46123. 46292, 48101. 48256, 60728. 60872,
63412. 63761, 65955. 66099, 69934. 70050, 73043. 73183,
83879. 84141, 85679. 85775, 86988. 87008, 96451. 96731)
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FLTMLTAIATQGAISRETQNGYYVKSYKLEVSTNGEDWMVYRHGKNHKVFQANNDATE
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IPHVGPLIGKYCGTKTPSELRSSTGILSLTFHTDMAVAKDGFSARYYLVHQEPLENFQ
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YPQDYPSHQNCEWIVYAPEPNQKIVLNFNPHFEIEKHDCKYDFIEIRDGDSESADLLG
KHCGNIAPPTIISSGSMLYIKFTSDYARQGAGFSLRYEIFKTGSEDCSKNFTSPNGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLLMVIREDQGGEWKHGRIILPSYDMEYQIVFEGVIGKGRSGEIAIDDIRISTDVFLE
NCMBPISAFAGGTLLPGTEPTVDTVÞMQPIPAYMYYVMAAGGAVLVLVSVALALVLHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRFRYAAKKTDHSITYKTSHYTNGAPLAVEPTLTIKLEQDRGSHC"
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note="receptor for VEGF165 and semaphorins class3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGAAACCAGGAAGGCTGGGCACCCTCCGTGGGCCTCACCCTCATTTGGAA 66659
                                                                                                                                                                                                                                                                                                                                                                                                        GI:10801453
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Pred. No. 36;
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3 (bases 1 to 116039)
3 (bases 1 to 116039)
Waterston,R.H.
Direct Submission
Submitted (15-JUL-2000) Genome Sequencing Center, Washington
Submitted (15-JUL-2000) Genome Sequencing Center, Washington
                                                                                                                                Direct Submission
Submitted (16-ARR-2005) Genome Sequencing Center, Washing
University School of Medicine, 4444 Forest Park Parkway,
MO 63108, USA
On Oct 14, 2000 this sequence version replaced gi:921135;
                                                                                                                                                                                                                                                         Direct Submission
Submitted (29-OCT-2002)
University, 4444 Forest
7 (bases 1 to 116039)
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Submitted (14-OCT-2000)
University, 4444 Forest
5 (bases 1 to 116039)
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Submitted (23-APR-1999) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                           MO 63108, USA
6 (bases 1 to 116039)
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Direct Submiss
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                                                                                                                                       Oct 14, 2000 this sequence version replaced gi:9211352.
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Center project name: H_NH0150F11
                  ----- Summary Statistics
                                   Contact: submissions@watson.wustl.
                                                          Web site: http://genome.wustl.edu
                                                                            Center: Washington University Genome Center code: WUGSC
                                                                                                                    ----- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                          Submission
                                                                                                                                                                                                                                                                                Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA
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                                                                                                                                                                                                 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Louis,
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                                                                                                                                                                                Fours,
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SGC

#### NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

### MAPPING INFORMATION:

Ś 밁 Ś ORIGIN

밁

Pocas

SOURCE

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

### SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5::1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org pBACe3

# NEIGHBORING SEQUENCE INFORMATION:

clone sequenced to the left is RP11-325M10, 200 base pair

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ACCESSION
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Best Local Similarity 64.8%;
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                                                                                                                                                                                                                                                                                                                      77259
                                                                                                                                                                                                                   77199
                                                                                                                                                                                                                                                                64 GGAGGCGAGGGAGCCTCCTGAGGCAGGGCCA 94
           Bos taurus clone CH240-54I8, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                         4 GCCCTGCCTCAGAAAACAGAAGGACGCAGCACACTCACGGTGACTCACCCCCATGTGGCT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overlap; the clone sequenced to the right is RP11-394E1, 200 base pair overlap. Actual start of this clone is at base position 117994 of RP11-325M10; actual end is at base position 115845 of
                                                                                                                                                                                                                TGATGAGAGGTGTTCCCCAAGGCCTGGGCCA 77169
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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CNVPLGMESGRIANEQISASSTYSDGRWTPQOSRLHGDDNGFFPHLDSNKEYLQVDLR
FLTMLTAIATQGAISRETQNGYYVKSYKMTPQOSRLHGDDNGFFPHLDSNKEYLQVDLR
FLTMLTAIATQGAISRETQNGYYVKSYKSTNGEDDMVYRHGKNHKVFQANNDATE
VVLNKLHAPLLTRFVRIRPQTMISGIALRLELFGCRVTDAPCSNMLGMLSGLIADSQI
SASSTQEYLWSPSAARLVSSRSGWFFRIPQAQPGEEWLQVDLGTPKTVKGVIIQGARG
GDSITAVEARAFVRKFKYSYSLNGKDWEYIQDFRTQPELFEGNMHYDTPDIRRFDFI
PAQVRHVPERRSPAAGIGMRLEVLGCDWTDSKETTVFTGFAFT
ECGENCSFEDDKDLQLPSGFNCNFDFLEEPCGWNYDHAKWLRTTWASSSSPNDRTFPD
DRNFLLQSDSQREGGYARLISPPVHLEFSFVCMEFGYQATGGRGVALQVVREASQES
UNITATEDDSCREGGYARLISPPVHLEFSFYCMEFGYGATGGRGVALQVVREASQES
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This gene was based on gi(4505458)
Continues as H_NH0394E01.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15626. .17342
/gene="NRP2"
/note="CpG_island (%GC=64.9, o/e=0.68, #CpGs=145)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / translation="Momeplitavpelaly peshqueqopdppcggrlnskdagy itspg
ypodypshoncemivyapepnoky ulipnpheelekhockyde is irdgisesadilg
khcgniapptiissggmiyiretsbuxapogageslrye krtgsedckkydheldindg
espgppekyphnldctftilakpkmeiilogflifdlehdplqvgegdckydhldindg
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54535 .54690,56663 .56832,58641 .58796,71269 .71413,
73953 .74302,76496 .76640,80475 .80591,83585 .83725,
94424 .94686,96224 .96320,97533 .>97553)
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/product="unknown"
/protein_id="AAX93216.1"
/db_xref="GI:62702291"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="NRP2"
/note="Homo aapiens neuropilin 2 (NRP2), mRNA.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="CpG_island (%GC=70.3, o/e=0.84, #CpGs=108)"
14041. .97553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="NRP2"
join(14041. .14113,28294.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LWVIREDQGGEWKHGRIILPSYDMEYQIVFEGVIGKGRSGEIAIDDIRISTDVPLE
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_xref="taxon:9606"
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5. .54690,56663. .56832,58641. .58796,71269. .71413,
5. .74302,76496. .76640,80475. .80591,83585. .83725,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39.8; DB 8; Pred. No. 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anylebechi, V., Ayagi, A., Ayodeji, M., Han, A., Mighald, V., Alpylebechi, V., Ayagi, A., Ayodeji, M., Barnstead, M., Benahmed, F., Biswalo, K., Blait, J., Blankenburg, K., Blyth, P., Brown, M., Benyll, M., Brantstead, M., Benahmed, F., Biswalo, K., Blait, J., Blankenburg, K., Blyth, P., Brown, M., Benyll, M., Brynt, M., Bhay, C., Burch, P., Burrell, K., Calderon, E., Chu, J., Claveland, C., Chockerll, R., Cox, C., Coyle, M., Cree, A., DySouza, L., Davis, C., Deramon, S., Deramo, C., Ding, Y., Dinh, H., Diyya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Franer, C.M., Gabisi, A., Ganta, R., Gardy, M., Guerra, W., Guerra, W., Gurrandez, S., Finley, M., Falgy, M., Forbes, L., Fosterr, M., Guevra, W., Gurrandez, S., Finley, M., Haddin, S., Henderson, N., Hernandez, M., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, M., Guerra, W., Guevra, W., Guerra, W., 
Direct Submission
Submitted (01-JUL-2005) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jun 28, 2005 this sequence version replaced gi:62543289. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                      Submitted (13.APR-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 233561)
                                                                                                                                                                                                          Cow Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 233561)
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 233561)
                                                                                                                                                                                                                                                                                                                                                                                     Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                          Department
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and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 26 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: PDDS

Center clone name: CH240-5418

Center clone name: CH240-5418

Assembly program: Atlas 3.0;

Consensus quality: 226744 bases at least Q40

Consensus quality: 228422 bases at least Q30

Consensus quality: 228422 bases at least Q20

Estimated insert size: 229662; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                     141749
151344
151394
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154841
166900
166950
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140342
140392
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111152
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95527
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                   166899:
166949:
172623:
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                                                                                                                                                                                                                                                                                                                                                                                                     4: contig of 5210 bp in length
4: gap of 50 bp
9: contig of 4935 bp in length
9: gap of 50 bp
9: gap of 50 bp
9: contig of 8153 bp in length
6: contig of 4414 bp in length
6: contig of 4414 bp in length
6: contig of 4639 bp in length
6: gap of 50 bp
9: gap of 50 bp
9: gap of 50 bp
9: contig of 47670 bp in length
6: contig of 15268 bp in length
                                                                                                                                                                             i: gap of 89 bp
i: contig of 5430 bp in length
i: gap of unknown length
contig of 3747 bp in length
i: gap of 50 bp
i: contig of 1307 bp in length
                   gap of gap of contig
                                                                                                                                                                                                                                                                                                   contig of 15575 bp in length
of 50 bp
contig of 16674 bp in length
gap of 50 bp
contig of 3050 bp in length
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sequence.
AC124345
AC124345.4 GI:37361090
HTG.
Mus musculus (house mouse)
                                                        Mus musculus
                                                                   AC124345
                                                                                                                                                                                                                             Similarity
                                                                                                                                                 TGCAGAAGGTCCCTCGCAGTCATGAAACCAAGGGAAGGCTTGGGAAAAC
                                                                                                                                                                       GCCTGGCCAGGGATTAGCCTGCTGGTCTGAGGCTGGCCCCCACGTCCCAGCACTGCCCGC 125599
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226104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="CH240-5418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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ated_length=50
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                                                                                                                                                                                                                             Score 39.8;
Pred. No. 3:
                                                        184532 bp
RP24-459N19
                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n length
3 bp in length
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from
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Direct Submission

Submitted (02-OCT-2003) Genome Sequencing

Parkway, St. Louis, MO 63108, USA

Comparison of the Comparison
                                                                                          NEIGHBORING SEQUENCE INFORMATION: This sequence is the entire insert overlapped by AC021667.
                                                                                                                                                                                                        The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                 Mapping information for this clone was provided by Dr. Wes Warren, bepartment of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (27-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Oct 2, 2003 this sequence version replaced gi:27803375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19-JAN-2003) Genome Sequencing Center, Parkway, St. Louis, MO 63108, USA 5, (bases 1 to 184532)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Parkery, St. Louis, MO 63108, USA
4 (Dases 1 to 184532)
McPherson, J. D. and Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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McPherson, J.D. and Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi, Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                         SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAPPING INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 184532)
Dauphin, S. and Haakenson, W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: M_BB0459N19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://genome.wustl.edu
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                                                                 Location/Qualifiers
         /organism="Mus musculus"
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|26377. .126524
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27391. .27618
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/clone_lib="RPCI-24"
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/chromosome="15"
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.16901. .116956
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)553. .9657
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Search completed: March 25, 2006, 17:51:42 Job time: 3016.5 secs
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No.

#### SUMMARIES

Score Match Length DB 13 563 99 8 564 13 553 98 0 29340 13 553 98 0 29501 14 38.2 6.8 2161 8 A 38.2 6.8 2777 11 38.2 6.6 2777 11 38.2 6.6 1957 4 A 37.2 6.6 1957 9 A	7 37.2 6.6 1957 4	4	37.2 6.6 1957 9	37 6.6 1785 6	36.6 6.5 550 9	36.4 6.5 76180 13	36.2 6.4 138203 14	36 6.4 546 13	15 35.8 6.3 704 2	16 35.8 6.3 1263 6	The second secon	17 35.6 6.3 568 5	17 35.6 6.3 568 5 A 18 35.2 6.2 954 14	1 00	35.36.37.22.23.16	# A A A A A A A A A A A A A A A A A A A	Length 29340 29340 57501 57501 7127 712 712 712 712 712 712 712 712 7	; ,		<u> </u>	, to	00 00 000 1 00 1 00 00 00 00 00 00 00 00
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o. o	ص ح	6.0	6.0	6.1 3	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.1 2	6.1 2	6.1 2	6.1		6.2	6.2	6.2	6.2	6.2	6.2	6.2
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		Ach71544 Human gen	Adb68842 Minority	Abq81844 Bifidobac	Adn60624 Human sec	Adg78333 Human sec	Acd18942 Novel hum	Aax85016 Human sec	Abq88096 Human ost	Adq39152 Human SNP	Adq39151 Human SNP	Ada71938 Rice gene	Ads56480 Bacterial	Adr52737 Drug ther	Abk84798 Human cDN	Aal38337 Complemen	Aak79886 Human imm	Aak68089 Human imm	Adr62531 Cotton cD	Ada71938 Rice gene	Adb60581 Connectiv	Aal07455 Human rep	Abk42425 Genomic s	Adp48674 Human Pel	Ab158452 Human pel

### ALIGNMENTS

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Human; ds; fibroblast growth factor-3; FGF-3; promoter; SNP; single nucleotide polymorphism; cancer; oesophageal cancer; 5'UTR; breast cancer; ovarian cancer; prostate cancer; head and neck cancer; oesophageal squamous cell carcinoma.
                                                                                                                                                                                                                     Human fibroblast growth factor (FGF) - 3 promoter 5' proximal
                                                                                                                                                                                                                                                                                   27-JAN-2005
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                     ADT97901;
                                                                                                                                                                                                                                                                                                                                                                                                                ADT97901 standard; DNA; 564 BP.
                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                        region.
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Key variation Location/Qualifiers replace(69,Y) /\*tag= a /standard\_name= "Single nucleotide polymorphism" /note= "This SNP is specifically claimed in claim 6"

US2004219582-A1.

04-NOV-2004.

11-MAR-2004; 2004US-00798652

17-MAR-2003; 2003US-0455689P.

(GUOY/) GUO Y.

Guo Y;

WPI; 2004-794435/78.

Novel isolated nucleic acid molecule having single nucleotide polymorphism in upstream untranslated region of fibroblast growth factor-3 gene, useful for assessing related susceptibility of mammal to cancer.

Claim 1; SEQ ID NO 1; 15pp; English.

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The invention relates to an isolated nucleic acid molecule comprising the upstream untranslated region (UTR) of fibroblast growth factor (FGF)-3 CC gene sequence (ADT97901) with a single nucleotide polymorphism (SNP) at CC position 69. Also included are an isolated nucleic acid molecule comprising a sequence complementary to ADT97901, a vector comprising the CC ADT97901 operably linked to a reporter gene, a host cell comprising the CC anticked asample from the mammal, and determining whether a cytosine CC or thymine is present at position 69 of ADT97901), a kit for performing CC the method (comprising a first oligonucleotide probe which anneals specifically with the target portion of the mammal's genome, where the first position of the mammal's genome, where the resparate nucleotide residues and the target portion includes the nucleotide residue located at position 69 of ADT97901, and a pair of primers for amplifying a reference portion of the CC ADT97901, and a pair of primers for amplifying a reference portion of the CC aligonucleotide probe that can anneal with a target portion of a mammal's genome, where the target portion includes the nucleotide residue one CC oligonucleotide probe that can anneal with a target portion of a mammal's genome, where the target portion includes the nucleotide residue one CC at position 69 of ADT97901. The method is useful for detecting SNP in FGF c3 gene in a mammal, preferably a human, and is also useful for assessing the relative susceptibility of a mammal to cancer (especially osephageal cancer), which shows an association with the presence of the C-allele. C cancer), which shows an association with the presence of the C-allele. C cancer is chosen from osesphageal, breast, ovarian, prostate, head can dneck cancer. The osesphageal cancer is chesen sequence is the upstream untranslated region (UTR) of fibroblast growth factor (FGF)-3 gene sequence.
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Query Match Sequence 564 BP; 117 A; 160 C; 185 G; 101 T; 0 U; 1 Other; 99.8%; Score 563; DB 13; Pred. No. 9.7e-142; Length 564;

Local

Similarity

S S S 밁 Ś 밁 밁 5 밁 Ś 밁 δ 밁 S 밁 밁 Matches 563; 361 361 301 301 241 181 481 421 421 241 181 121 121 61 61 ۲ AGCACTGCCCGCCGCCTCTGCGATGCAGTCCTCCTGGCCACCTGAGAACAGCCTGTAGAG 540 GGCTGGGCTGGGCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCC CCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGG CCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGG GCCGGCCATGCCCCAACGTTGCACACTCACTGCCTTTGCAGGGTTGGGGGCTTCCAGTC GCCGGCCATGCCCCCCAACGTTGCACACTCACTGCCTTTGCAGGGTTGGGGGCTTCCAGTC CTGGTGCCAGCCTCTGGAAGTCTGGAAGTGAGCAATGTTTCCCCATTAAGGAAAGTGTGTG CTGGTGCCAGCCTCTGGAAGTCTGGAAGTGAGCAATGTTTCCCCATTAAGGAAAGTGTGTG GGGGTCTTGCCATGGTGGGCACAGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCC GCAGCCCTGCCTCAGAAAACAGAAGGACGCAGCACACTCACGGTGACTCACCCCCATGTG ACAGGGTCCCATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAA ACAGGGTCCCATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAA Conservative 0 Indels 0; Gaps 180 120 480 420 420 360 360 300 300 240 240 180 60 480

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Morris DW, Malandro MS, 17-DEC-2002; 2002US-00322281 15-DEC-2003; 2003WO-US040081 (SAGR-) SAGRES DISCOVERY INC

Claim 16; SEQ ID NO 642; 182pp; English. Novel human cancer associated protein encoded within open reading frame of cancer associated gene, useful as targets for diagnosing cancer.

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The invention relates to cancer-associated proteins (CAP) and the cancercassociated (CA) nucleic acids encoding them. The invention also relates
cassociated (CA) nucleic acids encoding them. The invention also relates
cancer associated for treating cancers involving administering to a patient an
cancer inhibitor of CAP, and a method of screening for anticancer activity in a
cancer contacting a tissue sample derived from a cancer cell with an anticancer
cancer andidate and monitoring the effect of the anticancer drug candidate
cancer associated with expression of a CAP proteins are useful for detecting
cancer associated with expression of a CAP protein in a test cell sample
cand for screening for a bloactive agent capable of modulating the
cancer, involving determining the expression of a CA nucleic acid in a
cuissue. This sequence represents a human CA gene of the invention. Note:
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cuissue. This sequence represents a human CA gene of the invention. Note:
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concerning the cancer involving determining the expression of

Sequence 29340 BP; 6351 A; 8588 C; 8017 G; 6384 T; 0 U; 0 Other;

á 밁 ঠ 맑 묽 Ś Matches 564; Conservative Best Local Similarity Query Match 3686 121 1 GCAGCCCTGCCTCAGAAAACAGAAGGACGCAGCACACTCACGGTGACTCACCCCCATGTG GGGGTCTTGCCATGGTGGGCACAGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCC 180 GCAGCCCTGCCTCAGAAAACAGAAGGACGCAGCACACTCACGGTGACTCACCCCCATGTG 98.0%; Score 553; DB 13; Pred. No. 1.4e-138; 0; Mismatches 0; Length 29340; ŗ Gaps 3685 3625 3745 60

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541 481

AGGCAGTGGCGTCTTTCGGACTTC

AGCACTGCCCGCCGCCTCTGCGATGCAGTCCTCCTGGCCACCTGAGAACAGCCTGTAGAG

540

181

CTGGTGCCAGCCTCTGGAAGTCTGGAAGTGAGCAATGTTTCCCATTAAGGAAAGTGTGTG

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RESULT 3
ADZ13482
ID ADZ13482
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XX D7-J
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PN W01)
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The invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of screening for anticancer activity, a method of detecting a CA nucleic acid, a method of diagnosing cancer, a
                                                                                                                                                                                                                                                   The invention relates to a nucleic acid array for detecting a cancer associated (CA) nucleic acid, comprising two or more nucleic acid pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm; cytostatic; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                         acid array useful for detecting cancer es two or more nucleic acid probes.
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RESULT 4
ABX34807/c
ID ABX348
XX
AC ABX348
XX
DT 13-FEB
XX
XX
DE Human |
XX
XW MDDT;
KW anti-i

mddt

CDNA SEQ ID

368.

(first

ABX34807

standard; cDNA; 2161

ВP

MDDT; human; disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; osteopathic; cytostatic; ant

anti-HIV;

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     method of treating cancer and a method of inhibiting expression of a CA nucleic acids in a cell. The CA nucleic acids are useful for detecting CA nucleic acids. The antibody is useful for detecting the presence or absence of cancer cells in an individual which involves contacting cells from the individual with the antibody and detecting a complex of a CA protein from the cancer cells and the antibody, where the detection of the complex correlates with the presence of cancer cells in the individual. The composition is useful for inhibiting growth of cancer cells in an individual or for delivering a therapeutic agent to cancer cells in an individual. The invention is also useful for diagnosing cancer, for treating cancer and for inhibiting expression of a CA gene in a cell. This sequence represents human cancer-associated genomic DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 57501
                                                            4196
                                                                                                                       4136
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GAGGCAGTGGCGTCTTTCGGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGCCCTGCCTCAGAAAACAGAAGGACGCAGCACCCCCACGGTGACTCACCCCCCATGTG
                                                                           A-GCACTGCCCGCCGCCTCTGCGATGCAGTCCTCCTGGCCACCTGAGAACAGCCTGTAGA
                                                                                                                                                                                                  CCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGG
                                                                                                                                                                                                                                                            ACAGGGTCCCATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAA
                                                                                                                                                                                                                                                                                                                     GCCGGCCATGCCCCCAACGTTGCACACTCACTGCCTTTGCAGGGTTGGGGCTTCCAGTC
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Pred. No. 1.7e-138;
0; Mismatches 0;
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                                                                                                                                                                                                                                                        polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, correspathic, cytostatic, anti-inflammatory, immunosuppressive, anti-sender, anti-sender, nephrotropic, antipasamic, antipasoriatic and hepatotropic activity. The polynucleotides and the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polynucleotides are particularly useful for diagnosing, treating or preventing cell proliferative disorders (e.g. cancers including adenocarcinoma, cell proliferative disorders (e.g. cancers including adenocarcinoma, clawasemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's classase, acquired immunodeficiency syndrome (AIDS), Goodpasture's syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis. ABX34440-ABX34835 encode the MDDT polypeptides represented in SBU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU11450-ABU
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29-MAR-2001; 2001US-0280067P.
29-MAR-2001; 2001US-0280068P.
16-MAY-2001; 2001US-0291280P.
17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-0299428P.
20-JUN-2001; 2001US-0299776P.
20-JUN-2001; 2001US-0300001P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic; gene therapy; protein replacement therapy; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma anaemia; Crohn's disease; acquired immunodeficiency syndrome; ALDS; Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
                                                                                                                                                                                                                                                      Sequence 2161 BP; 354 A; 658 C; 708 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New purified disease detection and treatment molecule proteins polymucleotides, useful for diagnosing, treating or preventing (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, ostor hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 psoriasis; hepatitis; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dufour GE, Hillman JL,
Daugherty SC, Dam TC,
Peralta CH, David MH,
Flores V, Marwaha R, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-2002; 2002WO-US009944.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INCY-)
                                                                                                                                                                                                                                                                                              cification, but was obtained in electronic format from WIPO
.wipo.int/pub/published_pct_sequences
                                                                       1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  r GE, ...
nerty SC, Dam
nerty SC, Dam
nerty SC, David M
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                          139
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                                                                                                                                                                                      Similarity
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GCACAGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCCCTGGTGCCCAGCCCTCTGGA 198
                                                                       TCCGGCCCCAGAGGTGCCCACGTCTGGGGGGTCACTGCGGCAGCCAAGGCCTGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 368;
                                                                                                                 TCCTGAGGCAGGGCCAGGCAGCCGTCAGGTGGGTGACGGCAGGGGTCTTGCCATGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones AL,
                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    describes a novel disease
                                                                                                                                                                                   48.8%;
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JL, Yu JY, Tuason O,
C, Liu TF, Nguyen DA,
H, Lewis SA, Chen AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lo A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339pp + Sequence Listing; English
                                                                                                                                                              <u>,</u>
                                                                                                                                                                                      Score 38.2;
Pred. No. 5.
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                                                                                                                                                              Mismatches 108;
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Yap PE, Amsl
, Kleefeld Y,
, Panzer SR,
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Harris B;
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nting cancers
osteoporosis
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RESULT 5
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                                                                                                    Query Match
Best Local S
Matches 103
                                                                                                                                                                             The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The protectins ADM0759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence of the invention.
                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 578; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss; gene; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-APR-2002; 2002EP-00008400
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                                                                                                                 Similarity
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Yoshikawa T,
                                                                                                                                                         2777
                        GCACAGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCCCTGGTGCCAGCCTCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCACCGGAGCCCCACCCTGCGTGGTCCCACCCGGAGCATCGCTTGGGCCCCCGGCACTCAC
 CCACCGGAGCCCCACCCTGCGTGGTCCCACCCGGAGCATCGCTTGGGCCCCCGGCACTCAC
                                                   TCCGGCCCAGAGGTGGTGCCCACGTCTGGGGGGTCACTGCGGCAGCCAAGGCCTGGGGG
                                                                          rccreaeecaeecaeecaeccercaecreseaeaececaeecaecaecaecres
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                                                                                                                                                                                                                                                                                                                                                     and activity,
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                         BP; 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; diagnostic marker; pharmaceutical.
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                                                                                                               6.8%;
48.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Hio Y, Ot Otsuka M,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Otsuki T, Wakamatsu A,
Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, M
                                                                                                                                                                                                                                                                                                                                                     or as a target
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                                                                                                  Score 38.2; DB Pred. No. 5.5; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                     of gene
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K, Irie
Masuho Y;
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                                                                                                                              Length 2777;
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226
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cc a variety of human tissue sources and which encode novel secreted concluded are a vector complements and sequences that hybridise to them. Also cc included are a vector comprising the polynucleotide, a host cell cransformed with the vector, the proteins encoded by the polynucleotides, antibodies that bind to the proteins and identification of modulators of the proteins or the expression of the polynucleotide. The polynucleotides can be used as probes for the identification and isolation of full length cc cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The protein is useful in the treatment of the various immune deficiencies and disorders such as viral infections, concentrated arthritis, multiple sclerosis, autoimmune disorders (e.g. crhemmatoid arthritis, multiple sclerosis, autoimmune thyroiditis and conditions useful for treating neurodegenerative diseases (e.g. Alzheimer's calso useful for treating neurodegenerative diseases (e.g. Alzheimer's ce.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and cc (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and conditions are also useful for regulating haematopoiesis, for treating myeloid or calso useful for regulating haematopoiesis, for treating myeloid or compenses encoding a secreted mores!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
ABK34393/c
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Gulukota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacterial infection; fungal infection; autoimmune disorder; burn; rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis; diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour; coagulation disorder; haemophilia; inflammatory disorder; ulcer; tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Six hundred and twenty five polynucleotides derived f human tissue sources which encode secreted proteins, immune deficiencies and disorders such as autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Six hundred and twenty five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-179323/23
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sequences encoding a secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTTGCACACTCACTGCCTTTGCAGGGTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from a variety of , useful for treating e disorders.
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07-JUN-2000
28-JUN-2000
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11-JUL-2000
14-JUL-2000
26-JUL-2000
14-AUG-2000
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19-MAY-2000;
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17-MAR-2000;
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04-FEB-2000;
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69; Conserv
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2000US-022451BP.
2000US-0225213P.
2000US-0225214P.
2000US-0225267P.
2000US-0225267P.
2000US-0225268P.
2000US-02252768P.
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2000US-0214886P.
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2000US-0216647P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                tissue related disorder; cancer; gene therapy;
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Pred. No. 7.1;
0; Mismatches
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10-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                           The present invention relates to the isolation of novel human connective tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide (cDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides. Note: The sequence data for this patent did not form part of the printed specification, but the property of the printed specification, but the printed in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic
used in
                                                                                                                                                                                                                                                                            Sequence 1957
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69; Conser
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nilarity 56.6%;
Conservative
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2000US-0249211P
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2000US-025186P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding novel connective tissue associated polypeptides, nosing, preventing, treating or ameliorating a disorder such rheumatoid arthritis.
                                                                                                                                                                                                                                                                              BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID NO 1311; 673pp; English.
                                                                                                                                                                                                                                                                              515
                                                                                                                                                                                                                                                                            A; 580
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                                                                                                                                                                                                         0;
                                                                                                                                                                                                           Score 37.2; DB Pred. No. 9.3; 0; Mismatches
                                                                                                                                                                                                                                                                            C; 441 G;
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                                                                                                      370
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22-AUG-2000
23-AUG-2000
23-AUG-2000
31-AUG-2000
31-SEP-2000
32-SEP-2000
32-SEP

2000US-0226868 2000US-022934P 2000US-022934P 2000US-022934P 2000US-022934P 2000US-022934P 2000US-022951P 2000US-023043P 2000US-0231242P 2000US-0231242P 2000US-0231242P 2000US-0231243P 2000US-0231244P 2000US-0231244P 2000US-0231244P 2000US-0231413P 2000US-0231413P 2000US-0232081P 2000US-0232081P 2000US-0232081P 2000US-0232081P 2000US-023308P 2000US-023308P 2000US-023363P 2000US-023583P 2000US-023583P 2000US-023637P 2000US-023637P 2000US-023637P 2000US-023637P 2000US-023637P 2000US-024677P 2000US-024677P 2000US-024677P 2000US-024677P 2000US-024677P 2000US-024652P 2000US-024652P 2000US-024652P 2000US-0246610P 2000US-0246611P 2000US-0246611P 2000US-0246611P 2000US-0246611P 2000US-0246611P 2000US-0246611P

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RESULT 8
AALO7453
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  07-JUN-2000
28-JUN-2000
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16-SEP-2000
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04-FEB-2000
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  S-0186528P

S-0188350P

S-01980350P

S-02198123P

S-02114886P

S-02116840P

S-02116840P

S-02116840P

S-0225216880P

S-022521488P

S-0225266P

S-0225266P

S-0225266P

S-0225268P

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S-0239343P

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2000US-0232081P.
2000US-023239P.
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2000US-0232401P.
2000US-0233065P.
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2000US-02363709P.
2000US-02363709P.
2000US-024671P.
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2000US-024671P.
2000US-024677P.
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RESULT 9
ADB60580
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Best Local 9
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11-DEC-2000;
05-JAN-2001;
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08-DEC-2000
gene therapy; ds; connective tissues disorder; rheumatoid arthritis; systemic lupus erythematosus; scleroderma, Sjogren's syndrome; cancer cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; cardiovascular disease; atherosclerosis; myocarditis; cardiopulmonary bypass complication; autoimmune disease; multiple sclerosis; allergic reaction; asthma; rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis; gastrointestinal disorder; inflammatory bowel disease; organ transplant rejection; immune system disorder; Bruton's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences (number of human reproductive system related antigens. These can hin the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encorprotein of the invention
                                                                                                                                     cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular; antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritic; antiinflammatory; antiallergic; antiasterionatic; dermatological; nephrotopic; virucide; fungicide; antibacterial; antiparasitic;
                                                                                                                                                                                                                   Connective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGCCCATGCTGGCTCAGTTCCTGCCCCCTGGAGGGGAAGGGGGCCGAGGGGCTTCCTGTCCC
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2000US-0250391P.
2000US-0251030P.
2000US-0251988P.
2000US-0256719P.
2000US-0251856P.
2000US-0251868P.
2000US-0251868P.
2000US-0251869P.
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                                                                                                                                                                                                                   related genomic DNA #323.
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Pred. No. 9.3;
0; Mismatches
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                                                                                                          cancer;
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be used
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14 AUG-2000

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18 AUG-2000

22 AUG-2000

23 AUG-2000

30 AUG-2000

01 SEP-2000

01 SEP-2000

01 SEP-2000

05 SEP-2000

06 SEP-2000

06 SEP-2000

08 SEP-2000

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08 SEP-2000

09 SEP-2000

14 SEP-2000
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14-AUG-2000;
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14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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B-cell lymphoproliferative disorder; HIV; AIDS; inf
chromosome identification; chromosome mapping;
connective tissue related polynucleotide; gene; ds.
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17-MAR-2000;
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 2000US-018464P

2000US-018987P

2000US-0199076P

2000US-0199179P

2000US-021513P

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2000US-02151880P

2000US-0217487P

2000US-021748P

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2000US-022194518P

2000US-0225211P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
17-JAN-2001;
                                                                                                                         Human; single nucleotide polymorphism; SNP; MPL; chromosome 1p34; myeloproliferative leukaemia virus oncogene; haplotyping; genotyping; congenital amegakaryocytic thrombocytopaenia; CAMT; ds.
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P-PSDB;
               intron
                                                                                                                                                                               Reference sequence for human MPL
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neoplasias.
                                                                                                                                                                                                            26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                    ŊΞ
                                                                                                                                                                                                                                                                                                                                                                                                           ATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAACCAAGGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                           Ruben SM,
                                                                                                                                                                                                                                                                                                                                                               372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1311; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 2000US-0251990P.
; 2000US-0254097P.
; 2001US-0259678P.
; 2001US-00764847.
                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            describes
/number= 9
774. .1027
/*tag= b
                                                     Location/Qualifiers 614. .773
                                        /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , 26.68;
26.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37.2; DB Pred. No. 9.3; 0; Mismatches
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                                                                                                                                                                               gene
                                                                                                                                                                               exons 9-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 % identical to a connective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
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Gaps

310 224

370

08-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

21-SEP-2000 25-SEP-2000 25-SEP-2000 27-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 20-CCT-2000 02-CCT-2000 03-CCT-2000 04-NOV-2000 08-NOV-2000 08-NOV-2000

17-NOV-2000 01-DEC-2000 01-DEC-2000 05-DEC-2000 05-DEC-2000 06-DEC-2000 08-DEC-2000 08-DEC-2000 08-DEC-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specific oligonucleotides (ASOs) as probes and primers and/or primer-
extension oligonucleotides for detecting MPL gene polymorphisms. The
polynucleotides and screened repropunds are useful for the treatment of
diseases associated with MPL activity, such as congenital amegakaryocyt
thrombocytopaenia (CAMT). The present sequence represents a reference
sequence for human MPL gene exons 9-10. Note: This sequence encodes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chew
                           17-APR-2003
                                                                           US2003073623-A1
                                                                                                                                                                                                                                                              Human adult ovary cDNA #3455.
                                                                                                                                                                                                                                                                                                                  13-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                         ACH25075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1785 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel single nucleotide polymorphisms (SNPS) in the human myeloproliferative leakemia virus oncogene (MPL) gene located on chromosome 1p34, and methods for haplotyping and/or genotyping the MPL gene. The methods of the invention make use of allele-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; Fig 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-APR-2000; 2000US-0197839P
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                                                                                                                                                                                ss; sequencing by hybridisation; SBH; expressed
mapping; biodiversity; genetic disorder.
                                                                                                                                                                             mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGACGGCAGGGGTCTTGCCATGGTGGGCACAGG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choi JY,
                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAGGGCGGGCTCCGGCCCGGGTGGGCCGAAG 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Of.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the MPL protein shown in AAU09495
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*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA; 550 BP
                                                                                                                                                                                                                                                                                                                  entry)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stephens JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 T; 0 U; 3 Other;
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                                                                                                                                                                                                           sequence tag; EST;
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The invention relates to an isolated polynucleotide comprising any one of C38043 cDNA sequences, appearing as ACH1789-ACH50831, whose sequence was C4 determined by the technique of SBH (sequencing by hybridisation). Also C4 included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences cidentifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations cresponsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisones DNA or RNA. The purified polypeptide is one of the 3043 isolated CDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was contained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 12287; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-615964/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LABA/)
(STAC/)
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                                 seqdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LABAT I.
STACHE-CRAIN |
DICKSON M C.
JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Labat I,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones LW;
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Sequence 550 BP; 112 A; 142 C; 159 G; 132 T; 0 U; 5 Other;

DB

Length 550;

Ś Matches Query Match Best Local ocal Similarity 30 CAGCACACTCACGGTGACTCACCCCCATGTGGCTGGAGGGCGAGGGAGCCTCCTGAGGCAG 75; Conservative 6.5%; Score 36.6; DB Pred. No. 9.6; 0; Mismatches <u>,</u> 69; Indels 0 Gaps 89

S В Ś В 146 150 GCATACAGCTTACTCAGTGACAAT 173 206 CÁGCAGGCATTGCGGGCTCCATATTCATCGGGCTGAAGGCGAAGTAGCCCCCCGCAGGCTC 98 90 GGCCAGGGCAGCCGTCAGGTGGGTGACGGCAGGGGTCTTGCCATGGTGGGCACAGGGGCT 149 GGCCTGCCATGGATGGCGACGGATAAAGGAAAGGGNNTTCCNAGGGTTGTACAAGTGTCT 147 87

RESULT 12
ABD33385/c
ID ABD333
XX
AC ABD333
XX
DT 18-NOV
XX
DT Human
EN Human;
KW Human;
KW ds; ca
XX
OS Homo s ABD33385 standard; DNA; 76180 ΒP

Human cancer-associated (first entry) Ŝ gene HD07-071.

18-NOV-2004

ds; cancer; cytostatic. Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;

Homo sapiens

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RESULT 13
ADZ51725
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                                                                                                                                                                                                                                                                                                                                                                         The invention relates to cancer-associated proteins (CAP) and the cancer-
CC associated (CA) nucleic acids encoding them. The invention also relates
CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC cancer, involving determining the expression of a CA nucleic acid in a
CC cancer. This sequence represents a human CA gene of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                    Query Match
  gg
                                                                                          Streptomyces
                                                                                                                                                                                                                                                                                                                                                                     Sequence 76180 BP; 17603 A; 18463 C; 19657 G; 20457 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human cancer associated protein encoded within open reading f of cancer associated gene, useful as targets for diagnosing cancer.
                                                                                                            Antifungal; antiparasitic; polyketide; gene;
                                                                                                                                   FR-008
                                                                                                                                                       14-JUL-2005
                                                                                                                                                                                             ADZ51725 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-2003; 2003WO-US040081
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                                                                                                                                                                                                                                                  75706
                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; SEQ ID NO 492; 182pp; English.
                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                 polyketide gene cluster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DW,
                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                     GGACGCAGCACACTCACGGTGACTCACCCCCATGTGGCTGGAGGGCGAGGGAGCCTCCTGA
                                                                                                                                                                                                                                              GGAAGGGAGAGCGAGCCACCAGCGAGGTGACAGGTGACATC 75665
                                                                                                                                                                                                                                                                   GGCAGGGCCAGGCAGCCGTCAGGTGACGGCAGGGGTC 126
                                                                                                                                                                                                                                                                                        GGGGCCAGCCCTGGCATGGTGACTTTGGCAGATGGAGGAGAAGACACAGGAGCAGCGAGA
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                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                         sp.; FR-008
                                                                                                                                                      (first entry)
/product= "ADC lyase, PabC, complement (3150. .3818)
                             /product= "FAD-dependent monooxygenase,
complement(2264. .3037)
                                                          Location/Qualifiers
complement(574. .1950)
                                                   *tag=
                                                                                                                                                                                              DNA; 138203
                                                                                                                                                                                                                                                                                                                                       59.8%;
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Pred. No. 41;
0; Mismatches
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                                                                                                                                 SEQ
                                                                                                                                  ID
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          SEQ
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           ID
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                                        FBCO,
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 Lee SY,
                                                          23-OCT-2003; 2003KR-00074035
                                                                           06-APR-2004; 2004US-00819386
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                                       (KOAD)
                            KOREA ADV INST SCI & TECHNOLOGY. UNIV SHANGHAI JIAOTONG.
        Deng
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                                                                                                                                                                        complement (136558.
                                                                                                                                                                                                                                   /product= "PKS FscF, SEQ ID complement(84170. .107485)
                                                                                                                                                                                                                                                                                              /product= "PKS FscC, SEQ ID complement (60962. .77587)
                                                                                                                                                                                                                                                                                                                             complement (28983.
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/product= "ABC transporter,
27561. .28280
/******
                                                                                                                                                                                                                                                                                                                            /product= "ABC transporter, complement(28983. .60860)
                                                                                                                                                                                  product= "PKS FscD,
                                                                                                                                                                                                                                                                                                                                                                                       /product= "PKS FacA,
26333. .27340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Regulator protein,
complement(7210. .10320)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Regulator protein,
complement(4377. .7205)
                                                                                                                                                                                                     product= "PKS FscE, SEQ ID omplement(107496. .136148)
                                                                                                                                                                                                                                                               product= "PKS FecB, SEQ ID complement (77983. .84132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product= "Ferredoxin
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13522. .14898
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                                                                                                                                                                                                                                                                                                                                                                                                                                product= "ADC synthase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              product= "Thioesterase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product= "Cytochrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product= "GDP-ketosugar aminotransferase,
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         Chen S,
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    .16011
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                                                                                                                                                   "GDP-mannose-4,6-dehydratase,
       Jeong KJ,
                                                                                                                                                                       D, SEQ ID .137766)
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         Zhou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                             canine microarray; drug screening; toxicity assay; environmental pollutant; cellular response; gene expression profile; **cric response; liver necrosis; fatty liver disease;
                                                                                            Canis familiaris.
                                                                                                                                 toxic response; liver necrosis; fatty protein adduct formation; hepatitis;
                                                                                                                                                                                                                                Novel canine microarray-related
                                                                                                                                                                                                                                                                      21-OCT-2004
                                                                                                                                                                                                                                                                                                                                                   ADQ56739 standard; DNA; 546 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 138203 BP; 18153 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a gene cluster (ADZ51725) for the biosynthesis of FR-008 polyketides derived from Streptomyces sp. FR-008. FR-008 polyketide, a hetaene macrolide having adjycone containing 4-aminoacetophenone, has antifungal activity and also high toxicity against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   increasing the productivity 008 polyketide variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New gene cluster for the biosynthesis of FR-008 polyketides, useful increasing the productivity of FR-008 polyketides or to produce new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ADZ51726, ADZ51727, ADZ51728, ADZ51729, ADZ51730, ADZ51731, ADZ51732, ADZ51733, ADZ51734, ADZ51735, ADZ51736, ADZ51737, ADZ51738, ADZ51739, ADZ51739, ADZ51740, ADZ51741, ADZ51742, ADZ51743, ADZ51744, ADZ51745,
                                                        WO2004063324-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  109251
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                                                                                                                                                                                                                                                                    (first entry)
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Pred. No. 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                DNA sequence SeqID8041
                                                                                                                                 dog; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58;
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AAQ94044/c ID AAQ940 XX

AAQ94044 standard; DNA; 704 BP

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16-NOV-1995 AAQ94044;

(first entry)

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                                                                                                                                                                                                                                                                                                                                                              CC This invention is related to a novel isolated canine nucleic acid CC sequences and the construction of canine microarrays containing a CC significant portion of the canine genome. The isolated canine nucleic acid sequences of the invention may be useful for drug screening and containing the invention is therefore useful for assessing the coingact, including toxicity, of a compound, pharmaceutical agent or cenvironmental pollutant on a cell or living organism. The methods are useful for detecting genes that are up- or down-regulated in canines in a CC disease state. The sequences are useful as diagnostic agents or markers to detect a cellular response in a sample individually or as part of a gene expression profile. It is also useful as a target for agents that CC modulate gene expression or activity. The database is useful for producing electronic Northerns that allow the user to determine the cell type or tissue or cell. The methods are useful for determination of the abundance or expression level of a given gene in a compound or test agent will induce various specific compatible of a toxic response to one or more individual compounds. The methods are useful for determining the cell induced by a those of the toxins. The methods are also useful for predicting or elucidating the potential cellular pathways influenced, induced or that a teast one toxic response or the potential cellular pathways influenced, induced by the compound or test agent due to the similarity of the expression profile compound or test agent due to the similarity of the expression profile compound or test agent due to the similarity of the expression profile compound or test agent due to the similarity of the expression profile compound or test agent due to the similarity of the expression profile.
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                                                                                                                                                                                                                                                                                                                             Sequence 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-561890/54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-MAY-2003; 2003WO-US013853.
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                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                      CCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAACCAAGGGAGGCTTGGGAAA
NNNGCTGCTATCTTTGAGACAGA 150
                                      ACCAGGTCTGAGTCAGAGCCAGA
                                                                                CCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGGGGCTGGGCTGGGCAAGGCC
                                                                                                                                                                CCCACCCTGGCGNNGCCACAGCAGCCCNTCACGGCAANNAACCCNTGCAGCCTGGGGNCT
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                  BP; 96 A; 148 C; 161 G; 130 T; 0 U; 11 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO 8041; 41pp; English
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                                                                                                                                                                                                                                                                   50.3%;
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                                                                                                                                                                                                                                                Score 36; DB 1
Pred. No. 14;
0; Mismatches
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Best Local S
Matches 82
                                                                                                                                                                                                 The putative ALD gene identified in the distal part of chromosome Xq28 had deletions in 1 or several exons in 6 of 85 independent ALD patients examined. The gene has 10 exons and 9 introns, shown in AAQ94042-47
                                                                                                                                                                                                                                                                       New nucleic acid responsible for adreno-leuco-dystrophy - related probes, proteins and antibodies, useful for diagnosis and treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                        Sequence 704 BP; 127 A; 235 C; 205 G; 135 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                   WPI; 1995-215721/29.
                                                                                                                                                                                                                                                                                                                                         Mandel J, Aubourg P, Mosser J,
                                                                                                                                                                                                                                                                                                                                                                                                                                            16-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                  Claim 3; Fig 7B; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                   (INRM ) INST NAT SANTE & RECH MEDICALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ALD gene exon-3+4 region
                        610
                                                446
                                                                          670
                                                                                       386 CTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGGGGCTGGGCTGGGCAAGGCCACCAGG
506 CAGTCCTCCTGGCCACCTGAGAACAGCCTGTAGAGAGGC 544
                                                                                                                            82;
                                                                                                                        h 6.3%; Score 35.8; D
Similarity 51.6%; Pred. No. 17;
82; Conservative 0; Mismatches
                                           TCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCCAGCACTGCCGCCGCCGCCGCCTCTGCGATG 505
                       TCAGCACCTGCAGCAGCAGCAGGGGGGGGGGGTCACTCATAGGGAGGCGGACAGCCTTACCTC 551
                                                                       CAGAAGCACATGGAGGTCCCTGAGTGAGGGAGCGGGGATAGGAGGAGCTGGGGCAGCAGG
                                                                                                                                                                                                                                                                                                                                                                                          93CA-02108606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= f
/note= "base n at position 704 represents approx.
of intron-4 not given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= e
/label= Intron-4
/note= "150 bases of the intron-4 5'
704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Exon-3
295. .384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "base n at position 1 represents the 5' sequence of intron-2, not given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   554. .703
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/label= Exon-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Intron-3
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/note= "150 bases of the intron-2 3' sequence"
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                                                                                                                                                                                                                                                                                                                                          Sarde C;
                                                                                                                                                 DB 2;
                                                                                                                         77; Indels
                                                                                                                                               Length 704;
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Search completed: March 25, Job time : 476 secs 2006, 16:28:07

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Listing first
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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BD086268
AX003404
A57518
AR052984
AR306628
AR340054
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AX003404 Sequence
A57518 Sequence 10
AX052984 Sequence
AR306619 Sequence
AR306628 Sequence
AR340054 Sequence
AR340054 Sequence
AR3412123 Sequence
AR412123 Sequence
AR412123 Sequence
BD174200 Periplast
BD185155 Cell diff
AX817728 Sequence
AX817728 Sequence
AR57517 Sequence
AR096578 Sequence
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AR096578 Sequence
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AR533196	AR431659	AR210978	AR176959	AR163234	AR153219	AX610213	AR125635	AR125632	AR091430	AR091427	CQ862052	AR052978	AR052976	A57512	A57510	E51058	AX418821	AR373824	AR225902	AX958815	AX958559	AX010496	AR654868	BD210000	AR567736	AK442/98
AR533196	AR431659	AR210978	AR176959	AR163234	AR153219	AX610213	AR125635	AR125632	AR091430	AR091427	CQ862052	AR052978	7			E51058 A	AX418821	AR373824	AR225902	AX958815	AX958559	AX010496	AR654868	BD210000	AR567736	AK442/98
Sequence	Sequence	Sequence	Sequence	Sequenc	Sequenc	Sequenc	Sequence		Sequence 2	Attenuated	Sequence	Nucleic	Sequence	sequence												

#### ALIGNMENTS

RESULT 2
BD086268
LOCUS
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KEYWORDS
SOURCE REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM RESULT 1
AX701087/c
LOCUS
DEFINITION
ACCESSION
VERSION 밁 δ ORIGIN FEATURES Query Match Best Local S Matches 18 JOURNAL воигсе Vector. BD086268 BD086268.1 GI:22631878 JP 2001525168-A/21. synthetic construct 22 AX701087 Sequence 86 AX701087 μ 18; Ertl, P.F., Tite, J.P., van Wely, C.A. and Vaccine comprising gp120 and nef and/or against hiv
Patent: WO 03011334-A 86 13-FEB-2003;
GlaxoSmithKline Biologicals S.A. (BE);
Location/Qualifiers synthetic construct synthetic construct BD086268 other AX701087.1 Similarity CTCCCTCACCTCCAGCCACATG 22 CTTTCCCACCTCCTGCCACATG Conservative sequences; artificial sequences. /organism="synthetic construct" /mol\_type="unassigned DNA" /db\_xref="taxon:32630" /note="primer (figure 21)" GI:29536869 25 bp from Patent WO03011334. 70.9%; 81.8%; Score 15.6; DB 6; Pred. No. 2.6e+04; 0; Mismatches 4 22 å DNA DNA 6 Voss,G. GLAXO GROUP LIMITED Length 25; linear Indels linear the immunisation PAT PAT 0 27-AUG-2002 03-APR-2003 Gaps (GB) 0

AR105954

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REFERENCE
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RESULT 4
A57518
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MEDICAL RESEARCH COUNCIL

OS Artificial Sequence
PN JP 2001525168-A/21

PD 11-DEC-2001

PP 27-NOV-1998 JP 2000523326

PR 28-NOV-1997 GB 9725311.6, 28-NOV-1997 GB 9725313.2 P

20-MAR-1998 GB 9806072.6, 05-NOV-1998 GB 9824275.3 PI

SAMBING SHEW, ADDREAS SCHEDL, ANTHONY JOHN HARMAR PC

C12N15/09,C12N15/00

CC Description of Artificial Sequence: Primer
FH Key

FT Source 1. .22

/organism='Artificial Sequence'
                                                                                                                                                                                                                                                                                                                                                                                                      AX003404
Sequence 21
AX003404
A57518
Sequence :
A57518
A57518.1
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SCHEDL ANDREAS (DE); HARMAR ANTHONY
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/db_xref="taxon:32630"
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from Patent WO9928449.
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                         WO9632483.
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           Synthetic genes for plant gums
Patent: US 6548642-A 10 15-APR-2003;
Ohio University; Athens, OH
Location/Qualifiers
                                                           1 (bases 1 to 30)
Kieliszewski, M.J.
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Masucci, M.G.
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IMMUNE-EVADING PROTEINS
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Patent: WO 9632483-A 10 17-OCT-1996;
MASUCCI MARIA GRAZIA (SE)
Other publication AU 5284296 961030.
Location/Qualifiers
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Patent: US 5833991-A 16 10-NOV-1998; Location/Qualifiers Glycine-containing sequences conferring Score 14.6; DB 6; Pred. No. 7.5e+04; D; Mismatches 4 5833991. DNA" DNA 6, 6, invisibility to the immune Length Length Indels linear 24; PAT 29-SEP-1999 0 Gaps

0

Score 14.6; DB 6; Pred. No. 7.5e+04; 0; Mismatches 4 30 bp S 6548642. Indels linear PAT 12-JUN-2003 0 Gaps

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Patent: US 6570062-A 10 27-MAY-2003;
Ohio University; Athens, OH
Location/Qualifiers
                                                                                                                                                                       Unclassified.

1 (bases 1 to 30)

Kielszewski,M.J.

Synthetic genes for plant gums and other hydroxyproline-rich
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Sequence 10 from patent US
AR340054
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Patent: US 6548642-A 38 15-APR-2003;
Ohio University; Athens, OH
Location/Qualifiers
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Kieliszewski, M.J.
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          CACCTTCACCTCCACCCCAT 25
                        CTCCCTCACCTCCAGCCACAT 21
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                                                 66.4%;
nilarity 81.0%;
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                                                                                                  /organism="unknown"
/mol_type="unassigned DNA"
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81.0%; Pred. No. 7.4e+04;
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                                                 Score 14.6; DB 6;
Pred. No. 7.4e+04;
0; Mismatches 4;
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Pred. No. 7.4e+04;
0; Mismatches 4;
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S 6570062.
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S 6548642.
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AR412123
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AR412132
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Patent: US 6639050-A 10 28-OCT-2003;
Ohio University; Athens, OH
Location/Qualifiers
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Sequence
AR340063
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Sequence 38 from patent US
AR412132
AR412132.1 GI:40166776
                                                                                                                                                                                l Similarity
17; Conserva
                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 30)
Kieliszewski,M.J.
Synthetic genes for plant gums and other hydroxyproline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic genes for plant gums and other glycoproteins
Patent: US 6570062-A 38 27-WAY-2003;
Ohio University; Athens, OH
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               Unknown.
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/mol_type="unassigned
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Pred. No. 7.4e+04;
0; Mismatches 4;
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Pred. No. 7.4e+04;
0; Mismatches 4
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BD174200/c
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  KEYWORDS
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                                                                                                                                                                                                                                                                                         TAKEDA CHEMICAL INDUSTRIES LTD, YUKIKO HIKICHI, YASUSHI SHINTANI,
HIDEKI MATSUI

OS ARTIFICIAL Sequence
PN WO 02066049-A/46
PD 29-AUG-2002
PD 29-AUG-2002
PO 0205001536
PR 23-FEB-2001 WO 010 049450
PI YUKIKO HIKICHI, YASUSHI SHINTANI, HIDEKI MATSUI PC
A61X38/17, A61X31/711, A61X48/00, A61P43/00, A61P21/04, PC
A61P15/00,
PC C12N15/12,C07K14/47
CC Primer
FH Key
FT SOURCE
1. 21
/riganism='Artificial Sequence'.
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Kieliszewski,M.J.
Synthetic genes for plant gums and other hydroxyproline-rich glycoproteins
glycoproteins
patent: US 6639050-A 38 28-OCT-2003;
Ohio University; Athens, OH
Location/Qualifiers
2
Cell differentiating agent.
BD185155
BD185155.1 GI:31877355
JP 2002356438-A/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other sequences; artificial sequences.

1 (bases 1 to 21)

Hikichi,Y., Shintani,Y. and Matsui,H.
Periplastic converting agent
Patent: WO 02066049-A 46 29-AUG-2002;
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Periplastic converting agent.
BD174200
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WO 02066049-A/46.
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llarity 93.8%;
Conservative
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/mol_type="genomic |
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PF 21-PEC-2002

PF 21-FEB-2002 JP 2002044741

PI YUKIKO HIKICHI,/RASUSHI SHINTANI,HIDEKI MATSUI PC

A61K38/00,A61K31/7088,A61P15/00,A61P21/04,A61P35/00,C12N15/09// PC

C07K14/525,

PC C12Q1/68,A61K37/02,C12N15/00

CC Primer

FH Key

FT source

Location/C....
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1 (Dases 1 to 21)
Hikichi,Y., Shintani,Y. and Matsui,H.
Cell differentiating agent
Patent: JP 2002356438-A 46 13-DEC-2002;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Artificial Sequence
PN JP 2002356438-A/46
PD 13-DEC-2002
                                                                                                                                                                                                                                                                      Decristofaro, M.F., Padigaru, M., Miller, C., Tchernev, V., Zhong, H., Zhong, M., Anderson, D., Ballinger, R., Gerlach, V., Spytek, K.A., Rastelli, L., Kekuda, R., Guo, X., Zerhusen, B., Andrew, D., Mezes, P., Patturajan, M., Burgess, C.E., Eisen, A., Wolenc, A., Baumgartner, J., Shimkets, R.A., Gusev, V., Vernet, C.A., Taupier, R.J., Pena, C., Shenoy, S., Li, L., Casman, S., Bolgog, F., Fernandes, E., Smithson, G., Malyankar, U., Taillon, B. and Liu, X.

Novel polypeptides and nucleic acids encoded thereby Patent: WO 02081517-A 476 17-OCT-2002;
Curagen Corporation (US)
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Location/Qualifiers
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/note="Description of Artificia
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Pred. No. 9.4e+04;
0; Mismatches 1
                                                       Score 14.4; DB 6;
Pred. No. 9.4e+04;
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A57517/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
Search completed: March 25, 2006, 14:43:29 Job time : 962 Becs
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23 CCCGCACCTCCAGCTCCAT 5
                                                                                                                                                                                                                                                                                   unidentified unidentified unclassified sequences.
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Sequence 9 from Patent W09632483.
A57517
A57517.1 GI:3713375
                                                                                                                                                     /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                     PAT 03-MAR-1998
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 30
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N_Geneseq_21:*
1: geneseqn1980
2: geneseqn2900
3: geneseqn2001
4: geneseqn2001
5: geneseqn2002
6: geneseqn2002
7: geneseqn2002
8: geneseqn2002
9: geneseqn2002
11: geneseqn201
12: geneseqn201
13: geneseqn201
14: geneseqn201
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22
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393.619 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                           4996997 seqs, 3332346308 residues
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geneseqn2003bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

17 18 19	c 113	ი	C 21	Regult
14.4 14.4 14.2	1144.6666666666666666666666666666666666	15.2 15.2 14.6	20.4 15.6	Score
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	69.1 69.1 66.4	100.0 92.7 70.9	Query Match
221 24	2220000	222222222222222222222222222222222222222	222	Length
2 8 13	126111	220062	1111	DB
ADS74003 ABT33560 AAQ40923	ABL51730 ABL51739 ADU09143 ADU09116 ADU0916 AAL49623 ADM69088	AAX57861 AAC85242 ACH6883 ACH63009 AAV55821 ADY00944	ADT97906 ADT97907 ADT97907 ADB67764	ID
Ad874003 A. gossyp Abt33560 NOV forwa Aaq40923 Probe Pol	AAXZ/863 JNA encod Ab151730 HRGP rela Ab151739 Hydroxypr Adu09143 Ser-Hyp4 Adu09116 Hydroxypr Aa119623 Tumour di Adm69088 Human TAT	424	Adt97906 Human FGF Adt97907 Human FGF Adb67764 HIV-1 qp1	Description

WPI; 2004-794435/78

Guo Y;

(GUOY/)

GUO

11-MAR-2004; 2004US-00798652. 17-MAR-2003; 2003US-0455689P. 04-NOV-2004.

# ALIGNMENTS

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ADT97906 standard; DNA; 22 BP.

ADT97906;

27-JAN-2005 (first entry)

Human FGF-3 promoter 5' proximal region T allele probe.

Human; ss; fibroblast growth factor-3; FGF-3; cancer; oesophageal cancer; breast cancer; ovarian cancer; prostate cancer; head and neck cancer; oesophageal squamous cell carcinoma; PCR; probe; SNP; single nucleotide polymorphism.

Homo sapiens.

Key

Location/Qualifiers

/*tag= a
/mod_base= OTHER
/note= "modified with Vic (not defined)"

modified_base 2
/*tag= b
/mod_base= OTHER
/note= "G is covalently linked to a TAMRA moiety (6-carbotetramethyl-rhodamine)"

US2004219582-A1.
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RESULT 2
ADT97907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Comprising unicausiated region (VIK) of Indoctide polymorphism (SNP) at CC gene sequence (ADT97901) with a single nuclectide polymorphism (SNP) at CC comprising a sequence complementary to ADT97901, a vector comprising CC ADT97901 operably linked to a reporter gene, a host cell comprising the CC vector, detecting a SNP in the FGF-3 gene in a mammal (involves isolating a nucleic acid sample from the mammal, and determining whether a cytosine CC arcinemathod (comprising a first oligonucleotide probe which anneals CC specifically with the target portion of the mammal's genome, where the comprises a first fluorescent label and a first fluorescence CC quencher attached to its separate nucleotide residues and the target portion includes the nucleotide residue located at position 69 of ADT97901) and a pair of primers for amplifying a reference portion of the CC aligonucleotide probe that can anneal with a target portion of a mammal's gene, where the target portion includes the nucleotide residue located at position 69 of ADT97901 and a microarray having at least one CC genome, where the target portion includes the nucleotide residue located at position 69 of ADT97901. The method is useful for detecting SNP in FGF agene, which shows an association with the presence of the C-allele. The cancer is chosen from ocesophageal to cancer (sepecially ocesophageal CC and neck cancer. The ocesophageal cancer is cosophageal squamous cell ccl carcinoma. The present sequence is a Tagman PCR probe used to genotype individuals for the T SNP in the UTR of FGF-3.
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Best Local S
Matches 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecule having single nucleotide polymorphism in upstream untranslated region of fibroblast growth factor-3 gene, useful for assessing related susceptibility of mammal to cancer.
                                                                                                                                                                                                                                                                                Human; ss; fibroblast growth factor-3; FGF-3; cancer; oesophageal cancer; breast cancer; ovarian cancer; prostate cancer; head and neck cancer; oesophageal squamous cell carcinoma; PCR; probe; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 34; SEQ ID NO 6; 15pp; English.
                                                                        modified_base
                                                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22 BP; 4 A; 12 C; 2 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   upstream untranslated region (UTR) of fibroblast growth factor
                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADT97907 standard; DNA; 22
                                                                                                                                                                   modified_base
                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                FGF-3
                                                                                                                                                                                                                                                                    nucleotide polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                promoter 5'
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/mod_base= OTHER
/note= "G is covalently linked
carbotetramethyl-rhodamine)"
                                                                                             moiety
                                                                                               /mod_base= OTHER
/note= "C is covalently linked to
moiety (FAM)"
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                                                          *tag=
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Pred. No. :
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                       TAMRA moiety
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RESULT 3
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ID ADB677
XX ADB6776
XX ADB6777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule comprising upstream untranslated region (UTR) of fibroblast growth factor (FGF)-3 gene sequence (ADT97901) with a single nucleotide polymorphism (SNP)at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecule having single nucleotide polymorphism in upstream untranslated region of fibroblast growth factor-3 gene, useful for assessing related susceptibility of mammal to cancer.
                                       primer; ss
                                                                   HIV; Tat; HIV-1; Nef; gp120; vaccine; immunisation; human; anti-HIV;
                                                                                                                                      HIV-1 gp120 optimised sequencing primer g120c-SF4
                                                                                                                                                                                                                                                                                                                                                ADB67764 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCCCTCACCTCCAGCCACATG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 BP; 3 A; 12 C; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCCTCGCCTCCAGCCACATG 22
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                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                DNA;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                       15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of an HIV Tat, Nef or gp120 protein or polynucleotide in manufacturing a vaccine for a prime-boost delivery for the prophylactic or therapeutic immunization of humans against HIV.
                                autoimmune
                                            YAC; yeast artificial chromosome; PCR primer; sexual dysfunction; reporter gene; transgenic mammal; therapy; circadian function; sleep disorder; eating disorder; premenstrual syndrome; birth def
                                                                                                                                                                                                                       AAX57861 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                     PCR primer
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                                 disorder; ss.
                                                                                                                  used in construction of yeast artificial chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 6
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                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                               70.9%;
81.8%;
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Pred. No. 9.1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (YAC) vectors contain a reporter gene and transgenic mammals produced CC using them may be used to screen for an agent affecting nucleotide expression and gives easier monitoring of in vivo expression. The vector is used in the production of transgenic mammals for testing potential CC pharmaceutical or veterinary agents useful in treatment of disturbance of circadian function, sleep disorders, sating disorders, premenstrual CC syndrome, autoimmune disorders, birth defects in women and/or sexual CC disorders related to the expression pattern of a nucleotide such as those cC disorders related to the expression pattern of a nucleotide such as those above. The vectors have more concentrated YAC DNA, which allows better CC and more reliable gene transfer. The presence of a reporter gene allows ceasy monitoring of in vivo expression and the vectors allow for gene CC easy monitoring of in vivo expression and the vectors allow for gene CC easy monitoring of in vivo expression and the vectors allow for gene CC easy monitoring of in vivo expression and the vectors allow for gene CC easy monitoring of in vivo expression and the vectors allow for gene CC easy monitoring of in vivo expression and the vectors allow for gene CC easy monitoring of in vivo expression and the vectors allow for gene CC easy monitoring of in vivo expression and the vectors allow for gene CC coverexpression (3-5 fold) and easy site determination. The pyXM4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                Internal ribosomal entry site; IRES; yeast artificial chromosome; YAC; vector; centromere; telomere; origin of replication; transgenic; circadian function; sleep disorder; and disorder; premenstrual syndrome; autoimmune disease; birth defect; sexual dysfunction; serotonin transporter; VIP2 receptor; SERT; VIPR2; polymerase chain reaction; PCR; primer; amplify; YAC 35D8/D6;
                                                                                                                                                                                                                                                                                                                   AAC85242 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22
                                                                                                                                                                                                     Reverse primer D
                                                                                                                                                                                                                                             22-MAR-2001
                                                                                                                                                                                                                                                                                AAC85242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a PCR primer used in the construction of a yeast artificial chromosome of the invention. The yeast artificial chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 56; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New reporter gene labeled YAC vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-290603/25
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                                                    YAC HSC7E526/V12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-NOV-1997;
20-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           potential active agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                         (first entry)
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98GB-00006072.
98GB-00024275.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 A; 11 C; 0 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P
                                                                                                                                                                                                         26376 for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.1%;
                                                                                                                                                                                                                                                                                                                       ΒP
                                                                                                                                                                                                     determining size of YAC insert.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.2; DB 2;
Pred. No. 1.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Synthetic

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20-MAR-1998;
05-NOV-1998;
                                                          Gene expression analysis; array; hybridisation; genetic variation; tag-labelled compound; gene family; in situ hybridisation; library screening; Southern hybridisation; northern hybridisation; dot-blot hybridisation; gene sequence; mutation detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transgenic organism for identifying potential therapeutic agents able to modulate gene expression, comprises a yeast artificial chromosome vector.
                                            target sequence;
                                                                                                                                                                                 17-OCT-2003
                                                                                                                                                                                                                 ACH62883;
                                                                                                                                                                                                                                                  ACH62883 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22 BP; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         two nucleic acid sequences (e.g. NOI plus a reporter of more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schedl A,
                                                                                                                                                                                                                                                                                                                                     TTCATCACCTCCATCCACAT 20
                                                                                                                                                                                                                                                                                                                                                                     TCCCTCACCTCCAGCCACAT 21
                                                                                                                                              sequence #12019 useful in array
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                (first entry)
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97GB-00025313.
98GB-00006072.
98GB-00024275.
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                                            sation; gene sequence
probe; PCR; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; 11 C; 0 G; 6 T; 0 U; 0 Other;
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85.0%;
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Pred. No. 1.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                             88
                                                                                                                                              for genetic analyses
                                                                                                                                                                                                                                                                                                                                                                                                        ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 22;
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ACHGADA ACHGADA ID ACHG XX ACHG AC ACHG XX T17-C DT 17-C DT DNA XX DE DNA XX Gene KW tag-KW tag-KW 1ibb KW 1oct XX Gene KW tag-KW 1ibb KW 1carg XX Tag-XX Tag-XX

DNA target 17-OCT-2003

sequence

#12145 useful in array

for

genetic analyses.

(first entry)

ACH63009 standard; DNA; 25

Gene expression analysis; array; hybridisation; genetic variation; tag-labelled compound; gene family; in situ hybridisation; library screening; Southern hybridisation; northern hybridisation; dot-blot hybridisation; gene sequence; mutation detection;

gene sequence; mutation detection; PCR; primer; ss.

sequence;

probe;

밁 5

Matches Best Local

Similarity

Conservative

0;

Mismatches

Indels

0,

Gaps

0

Pred. No.

1.3e+04

w

CCCTCACCTCCAGCCACATG 22

CCTTCACGTCCAACCACATG 20

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The present invention relates to nucleic acid sequences that are complementary to particular genes, and can be used as probes for a crowaristy of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nucleotides from at least one of 14936 cumprises 9 or more consecutive nucleotides from at least one of 14936 cumprises 9 or more consecutive nucleotides from at least one of 14936 cumprises of a gene mismatch oligonucleotides. The probes may be used in an array comprising at least 10 distinct cumulate acid probes. The array is useful in monitoring gene expression converted by hybridisation to a DNA library, in analysing genetic cuseful for identifying family members of a gene. The probes are also useful for identifying family members of a gene. The probes are also cuseful for identifying family members of a gene. The probes are also cuseful for identifying family members of a gene. The probes are also cuseful for identifying family members of a gene. The probes are also cuseful for identifying family members of a gene. The probes are also cuseful for identifying family members of a gene. The probes are also cuseful for identifying family members of a gene. The probes are also cuseful for identifying family members containing segments of DNA 
                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New probe array useful e.g. for monitoring gene expression levels, for analyzing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes.
                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-AUG-2002; 2002US-00215112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003082596-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 12019; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-576608/54
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                                                                                   25
                                                                                BP; 6 A; 11 C; 4 G; 4 T; 0 U; 0 Other;
69.1%;
                            Score 15.2;
                               DB 9;
                         Length
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RESULT 8
AAV55821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC complementary to particular genes, and can be used as probes for a CC complementary to particular genes, and can be used as probes for a CC variety of analyses such as gene expression analysis. Each probe CC comprises 9 or more consecutive nucleotides from at least one of 14936 cm cleotide sequences defined in the patent, or their perfect sense match, CC sense mismatch, antisense match or antisense mismatch oligonucleotides. The probes may be used in an array comprising at least 10 distinct concleic acid probes. The array is useful in monitoring genetic concleic acid probes. The array is useful in monitoring genetic consecutions, and in hybridising tag-labelled compounds. The probes are useful for identifying family members of a gene. The probes are also cuseful in in situ hybridisations, in screening cDNA or genomic libraries consecutived subclones) for additional clones containing segments of DNA that have been previously isolated and sequenced, in Southern, northern, cc sequence of any gene or detect specific mutations in any gene, and in matched and sequences of the sequences of the invention are also useful as PCR primers. The invention provides a large collection of nucleic acid sequences confided the invention uses. CC complementary to particular genes with a wide range of analytical uses. CC complementary to particular genes with a wide range of analytical uses. CC directly from the USPTO web site at segdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 17
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analyzing
comprises
Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autoimmune disease; inflammation; nitro drug; IkappaB regulator protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; prodrug therapy; protease; cancer; pathological condition; minimal motif; PCR primer; ss.
                                                                                                                                   27-AUG-2003
18-NOV-1998
                                                                                                                                                                                                                  AAV55821 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                    Multimerisation
                                                                                                                                                                                     AAV55821;
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                                                                                                                                                                                                                                                                                                                                                                  l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                 CCCTCACCTCCAGCCACATG 22
                                                                                                                                                                                                                                                                                                  CCTTCACGTCCATCCACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                   25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                array useful e.g. for monitoring gene expression levels, genetic variations, or for hybridizing tag-labeled compo-multiple nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                   BP;
                                                                                                                                                                                                                                                                                                                                                                69.1%;
llarity 85.0%;
Conservative
                                                                                                                                  (revised)
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                                                                                                 of minimal motifs using
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                                                                                                                                   entry)
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0: Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               Score 15.2; DB 9; Length 25; Pred. No. 1.3e+04;
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U,
                                                                                                   primer ZGY2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   0 Other;
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PCR primer 170

(first entry) used

gynecology and obstetrics; neoplasm; cytostatic; metastasis;
gene therapy; RNA interference; UDP-galactose 4-epimerase; GALE;
UDP-glucose 4-epimerase; lysophospholipase; HT014; LOC148902; LYPLA2;

88

SNP detection; breast tumor; endocrine disease;

to amplify human GALE

region

SNP

Homo sapiens

PCr; primer.

RESULT 9

ADY00944 standard; DNA;

29

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                                                                                                                                          Course of the invention for the multimerisation of minimal motifs. The course of the invention for the multimerisation of minimal motifs. The course of the invention for the multimerisation of minimal motifs. The course of the invention for increasing the resistance of a core protein to proteolytic degradation that comprises linking or inserting core of the core protein a stabilising polypeptide of formula control or into the core protein a stabilising polypeptide of formula control of core protein a stabilising polypeptide of formula core residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr can do not not nepeat. Alternatively a nucleic acid encoding a stabilising core protein. The fusion proteins of the invention are more resistant to core protein. The fusion proteins of the invention are more resistant to degradation by proteases and, thus, have a longer half-life than the core diseases, cancer and inflammation. In particular, the core protein may be an IkappaB regulator protein for the treatment of inflammatory bowel considered core protein for the treatment of inflammatory bowel conserved in protein which can activate nitro drugs in caryme/products can also be used in diagnostic methods such as in the fusion proteins can also be used in diagnostic methods such as in
                                                                    Matches
                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fusion proteins resistant to proteolytic degradation - comprising a core protein with a stabilising polypeptide comprising a peptide sequence containing glycine repeats.
                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 72; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MASU/) MASUCCI
                                                                                      Local
                                                                                                                                                                        fusion proteins can also be used in diagnostic imaging. (Updated on 27-AUG-2003 to correct OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998-312463/27
                                                                  l Similarity 17; Conserv
                               CTCCCTCACCTCCAGCCACAT
                                                                                                                                          24
CACCCGCACCTCCAGCTCCAT
                                                                                                                                        BP;
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0030986P.
97US-0048945P.
                                                                                                                                        5 A;
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                                                                                 66.4%;
81.0%;
                                                                                                                                        13 C; 2
                                                                  ۰,
                                                                                   Score 14.6; DB 2;
Pred. No. 2.3e+04;
                                                                                                                                        G; 4 T; 0 U; 0 Other;
                               21
                                                                    Mismatches
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                                                                                                     Length
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                                                                    Gaps
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RESULT 10
AAX27663
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Best Local S
Matches 17
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25-NOV-2003;
25-NOV-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of breast cancer comprising detecting the presence or absence of a polymorphic variation associated with breast cancer. The method of the invention demonstrates cytostatic activity and may be useful for identifying a risk of, preventing and/or treating breast cancer and cancer metastasis. The methods may be utilized for gene therapy or RNA interference. The current sequence is that of a PCR primer of the invention which was used to amplify a human HT014/LOC14902/LYPLA2 (lysophospholipage I)/GALE (galactose-4-epimerase, UDP-) DNA containing the polymorphic primer of the containing the property of the pr
                                                            21-JUL-1997;
20-JUL-1998;
                                                                                                                         21-JUL-1998;
                                                                                                                                                                28-JAN-1999
                                                                                                                                                                                                                                                Acacia
                                                                                                                                                                                                                                                                                     glycopeptide;
                                                                                                                                                                                                                                                                                                      Synthetic gene; plant; gum; hydroxyproline-rich glycoprotein; HRGP; repetitive proline-rich protein; RPRP; arabino-galactan protein; AC
                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a HRGP motif.
                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying risk of, preventing and/or treating breast identifying and/or analyzing polymorphic variations in sequences within the human genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
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                      (UYOH-) UNIV OHIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to a novel method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCTCTCTCCTCCCTCCACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCCCTCACCTCCAGCCACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleotide polymorphism (SNP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nelson MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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2003US-00723681.
2003US-0525239P.
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                                                                                                                                                                                                                                                                                     88.
                                                            97US-00897556.
98US-00119507.
                                                                                                                           98WO-US015083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                          entry)
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for identifying a subject at risk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .3e+04;
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RESULT 11
ABL51730
ID ABL51730
ID ABL51730
ID ABL51730
AC ABL51
AC ABL51
AC ABL51
AC ABL51
AC PRGP
KW Plant
KW Plant
KW AGP;
XX AGac;
OS Syntl
XX
PD 25-00
XX
PD 25-00
XX
PD 12-A
XX
PR 112-A
XX
PR 11
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Best Local S
Matches 17
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                        The present invention describes synthetic genes encoding plant gums and other hydroxyproline (Hyp)-rich glycoproteins (HRGPs) and the nucleic acids that encode them. The nucleic acids, proteins and methods from the present invention may be used to produce HRGPs, repetitive proline-rich proteins (RPRPs) and arabinogalactan-proteins (AGPs) in plants via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30
                                                                                                                                                                                                                                       Nucleic acids and proteins useful glycoproteins in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein;
HRGP; repetitive proline-rich protein; RPRP; arabinogalactan protein;
AGP; plant gum; PCR primer; linker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel synthetic gene designed from repetitive hydroxyproline-rich glycoprotein.
                                                                                                                                                                                                                                                                                                                          WPI; 2002-041307/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acacia senegal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRGP related oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-APR-2000; 2000US-00547693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-APR-2001; 2001WO-US012336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-0CT-2001
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                                                                                                                                                                                      Page 4-5;
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81.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.6;
Pred. No. 2.
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                                                                                                                                                                                   English.
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Matches 17
                                                               Query Match
Best Local
                                                                                                                              The present invention describes synthetic genes encoding plant gums and other hydroxyproline (Hyp) rich glycoproteins (HRGPs) and the nucleic acids that encode them. The nucleic acids, proteins and methods from the present invention may be used to produce HRGPs, repetitive proline-rich groteins (RPRPs) and arabinogalactan-proteins (AGPs) in plants via recombinant methodologies. Also described is the expression of synthetic genes designed from repetitive peptide sequences, such as glycoproteins (including the peptide sequences of gum arabic glycoprotein (GAGP).

ABL51730 to ABL51849 and ABB78401 to ABB78544 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                         Nucleic acids and proteins useful for producing hydroxy-proline glycoproteins in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes designed from repetitive peptide sequences, such as glycoproteins (including the peptide sequences of gum arabic glycoprotein (GAGP)).

ABL51730 to ABL51849 and ABB78401 to ABB78544 represent sequences used the exemplification of the present invention
                                                                                                                                                                                                                                                                                 Example 2; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant; Gum arabic glycoprotein; GAGP; hydroxyproline-rich glycoprotein; HRGP; repetitive proline-rich protein; RPRP; arabinogalactan protein; AGP; plant gum; PCR primer; linker; ss.
                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                               Kieliszewski MJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydroxyproline-rich glycoprotein (HRGP) related linker SEQ ID NO:38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL51739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL51739
                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-APR-2001; 2001WO-US012336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200178503-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acacia senegal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                       CTCCCTCACCTCCAGCCACAT 21
                                                                                                       30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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CACCTTCACCTCCACCCCCAT
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                                                                                                      BP; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 6 A; 19 C; 0 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          OIHO
                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-00547693.
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                                                                                                                                                                                                                                                                                 53; 326pp;
                                                                                                      A; 19 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                               66.4%;
81.0%;
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81.0%;
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                                                                                                                                                                                                                                                                                 English
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                                                               Score 14.6;
Pred. No. 2.
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                                                  Mismatches
                                                                                                      5 T; 0 U;
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                                                                2.3e+04;
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                                                                           DB 6;
                                                                                                      0 Other;
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                                                                           Length 30;
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The invention relates to an isolated polypeptide (I) comprising confidered by contiguous hydroxyproline residues and the non-rigid modules are directed by contiguous hydroxyproline residues and the non-rigid modules care synthetic gums based on motifs and repeats found in Gum arabic glycoprotein (GAGP), Hydroxyproline-rich glycoproteins (AGP). Also cincluded are a polypeptide (II) (comprising a first elastin module having a first crosslinkage motif, and a second elastin module flanked on the C-terminal side by a first extensin module having a first crosslinkage motif, and a second elastin module flanked on the C-terminal comprises at least two contiguous hydroxyproline residues and is crosslinkage motif. The crosslinkage motif comprises a flycoprotein having a first crosslinkage motif. The crosslinkage motif comprises at least two contiguous hydroxyproline residues and is crosslinkage motif. The crosslinkage motif comprises at leastin module hydroxyproline residues and is crosslinkage motif. The crosslinkage motif comprises tyrosine forms an intramolecular or intermolecular crosslink. In polypeptide (II), the rigid module crosslinkage motif is Val-Tyr-Lys. The tyrosine forms an intramolecular or intermolecular crosslink. In polypeptide (II), the crosslinkage motif is val-Tyr-Lys and contiguous hydroxyproline residues. CI is repeated three times. The first and/or second crosslinkage motifs crist elastin module is repeated six times and the second elastin module. CI is repeated three times. The first and/or second crosslinkage motifs crist elastin module. The nucleic acid is equence and an internal lysine rich region. The variant encoded by the first and the second elastin modules. The Le-AGP-1 crist elastine modules. The polypeptide (II) is useful as a thickener, emulsifier, stabiliser, the polypeptide (II) is useful as a thickener, emulsifier, stabiliser. The crossensus motifs or repeat units derived from GAGP, AGP, RPRP or HRGP crossent derived conservation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant gums (especially gum arabic) useful in the food and cosmetics industries are produced by expression of synthetic genes designed f the repetitive peptide sequences of plant gum glycoproteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-2003; 2003US-00418032.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2004-784900/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gum; elastin; extensin; th:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 38; 179pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     extensin; thickener; emulsifier; stable fixative; food industry; cosmetic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Hydroxyproline-rich glycoprotein;
in; RPRP; arabinogalactan-protein; A
thickener; emulsifier; stabiliser;
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a polypeptide

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Sequence

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BP; 6

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19 C; 0

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Matches
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                                                                                                                                                                                                                             WPI; 2004-784900/77.
                                                                                                                                                                                                                                            Kieliszewski
                                                                                                                                                                                                                                                                                    13-APR-2004; 2004WO-US011174.
                                                                                                                                                                                                                                                                                                   04-NOV-2004
                                                                                                                                                                                                                                                                                                                WO2004094590-A2
                                                                                                                                                                                                                                                                                                                             Unidentified.
                                                                                                                                                                                                                                                                                                                                          repetitive proline-rich protein; RPRP; arabinogalactan-protein; plant gum; elastin; extensin; thickener; emulsifier; stabiliser; surfactant; flavour fixative; food industry; cosmetic; ss.
                                                                                                                                                                                                                                                                                                                                                              Gum arabic glycoprotein; GAGP; Hydroxyproline-rich
                                                                                                                                                                                                                                                                                                                                                                           Hydroxyproline-rich glycoprotein, HPGP, conserved motif DNA
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                                                                                                                                                                                                                                                                                                                                                                                                        ADU09116;
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCCCTCACCTCCAGCCACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                     SEQ ID NO 10; 179pp; English
                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
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Pred. No. 2.
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RESULT 15
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ID AAL496
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XX MOUSe;
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IN MOUSE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence and an internal lysine rich region. The variant encoded by the nucleic acid further comprises an enhanced green fluorescent protein fusion glycoprotein. The nucleic acid is expressed in Nicotiana tabacum. The polypeptide (I) is useful as a thickener, emulsifier, stabiliser, surfactant, or flavour fixative in the food industry. It is also useful in cosmetics. The polypeptide (I) has an anomalously low viscosity. The present sequence encodes a consensus motif or repeat unit derived from GAGP, AGP, RPRP or HRGP.
                                                                                                                                                                                                                                                       muscular dystrophy primer used in the
                                                                                                                                                                                                                                                                                                       The present invention relates to plasmic change agents with cell differentiation activity containing protein TL4. These can be used in treatment, prevention and diagnosis of rhabdosarcoma, lelomyosarcoma,
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmic change agents and antibodies to them for diagr of tumours of muscle tissue and of muscular dystrophy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hikichi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; tumour differentiation; rhabdosarcoma; leiomyosarcoma; rat; muscular dystrophy; uterine mvoma; cvtosratio, plaemio chance mr.
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                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Page 129; 136pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-2001; 2001JP-00049450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2002; 2002WO-JP001536
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                                                                                                                                                                                                    21 BP; 5 A; 2 C; 11 G; 3 T; 0 U;
                                                  CTCCCTCACCTCCAGC 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACCTTCACCTCCACCCCCAT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shintani Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 6
                                                                                                  Conservative
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                                                                                                                          93.8%;
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Pred. No. 2
                                                                                                                          Score 14.4; DB 6; Length 21; Pred. No. 2.7e+04;
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                                                                                                                       2.7e+04;
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                                                                                                                                                                                                                                                                               The present sequence
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Search completed: March 25, 2006, 19:02:17

Job time : 375.5 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. 18 the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

c 22	21	c 20	19	c 18	c 17	16	15	c 14		c 12		c 10	ი 9	ი 8	c 7	ი ი	ი თ	ი 4	ი ა	2	c 1	Result
11.6	11.8	11.8	12	12	12	12	12	12	12	12.2	12.2	12.2	12.6	12.6	12.6	12.8	13	13	13.2	13.6	14	Score
52.7	53.6	53.6	54.5	54.5	54.5	54.5	54.5	54.5	54.5		55.5	55.5	57.3	57.3	57.3	58.2	59.1	59.1	60.0	61.8	63.6	Query Match Length
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AZ453412	AZ592392	AZ348213	CZ477475	AZ788256	AZ332711	AZ462642	AI416870	AZ762096	AZ599021	AZ501699	AZ782026	AZ381798	CG730897	AZ785027	AZ778032	AZ498825	AA864650	AZ655652	AZ980990	D21049	CL676355	ID
		AZ348213 1M0084N15	CZ477475 d10866-3p	AZ788256 2M0035A17	AZ332711 1M0061N14	AZ462642 1M0269M09	AI416870 sa19b03.x	AZ762096 1M0556J18	AZ599021 1M0414F08	AZ501699 1M0340H12	AZ782026 2M0021123	AZ381798 1M0138G01	CG730897 1119130F0	AZ785027 2M0028H03	AZ778032 2M0013A11	AZ498825 1M0336J14	AA864650 oh37b09.s	AZ655652 1M0530D13	AZ980990 2M0258F17	D21049 HUMGS02034	CL676355 PRI0118b	Description

c 45	44	c 43	42	C 41	c 40	39	c 38	37	c 36	c 35	34	33		c 31				c 27	26	c 25	c 24	23
11	11	11	11	11	11	11	11	11	11	11	11	11	11.2	11.2	11.4	11.4	11.6		11.6	11.6	11.6	11.6
50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	0	50.9	50.9	51.8	51.8	52.7	52.7	52.7	52.7	52.7	52.7
29	29	28	28	27	26	25	25	25	24	23	22	19	29	23	25	24	30				23	22
9 AZ780387	9 AZ666737	9 AZ937148	8 N81476	9 AZ439789	10 CL650847	9 AZ348233	6 CF298174	1 AI620280	9 AZ404465	9 AZ654389	2 BG926061	1 AI538541	9 AZ812552	9 AZ374746	9 AZ471181	10 AG202658	9 AZ833458	9 AZ580965	9 AZ623416	9 AZ410218	9 AZ331349	8 D21051
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2M0017N12	1M05	2M0195A1	ESTZ	1M02	PRI	1MOO	7LEA	tu93	TOWL	1MOS	HNC23-1-	td08a11.	2M00	TOWL	1M02	Pan	2M01	1M03	1M04	1M01	DOMT	HUMGS02036
17N1	1M0549006	95A1	y47h(	30004	CL650847 PRI0110c	1M0084G04	7LEAF01	tu93e03.x	LM0172P09	1M0528H06	3-1-E	a11.x	2M0079K13	1M0127D15	1M0285H11	Pan trog	2M0115L02	1M0369C15	1M0461C08	1M0182F23	1M0059F17	2036

## ALIGNMENTS

Query Match Best Local : Matches 1	COMMENT FEATURES SOURCE ORIGIN	CLG76355/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM ORGANISM REFERENCE AUTHORS TITLE JOURNAL	ם הפוווית ן
Query Match 63.6%; Score 14; DB 10; Length 29; Best Local Similarity 100.0%; Pred. No. 2.4e+05; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ontact: Sommer RJ ontact: Sommer RJ volutionary Biology ax-Planck-Institute for Developmental Bi pemannstr. 37-39, Tuebingen D-72076, Ger el: 00497071601371 ax: 00497071601371 ax: 00497071601371 ax: 00497071601371 el: 10497071601371 mail: ralf.sommerstuebingen.mpg.de his library was generated at Caltech, Pa equenced at Vancouver, Canada. eq primer: T7 eq primer: T7 lass: fosmid ends. location/Qualifiers location/Qualifiers location/Qualifiers location-Qualifiers	PRIO1185 E09 2 - PRIO118b.BR (29) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic CL676355 CL676355.1 GI:50181863 GSS.  Pristionchus pacificus Pristionchus pacificus peristionchus pacificus Pristionchus pacificus Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.  1 (bases 1 to 29) Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppabB: an AcedB database for the nematode satellite organism Pristionchus pacificus Nucleic Acids Res. 32 (1), D421-D422 (2004)	

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RESULT
D21049
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                   JOURNAL COMMENT
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                                                                                        1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTCCCTCACCTCCAGCCACA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1993)
Contact: Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T.,
Yoshinari, H., Arimoto, J. and Matsubara, K.
Institute for Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 25)
Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Kojima, Y.,
Yoshinari, H., Arimoto, J. and Matsubara, K.
Gene expression of human promyelocytic cell line HL60 before and
after induction of differentiation. A new application of 3'directed
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                              2M0258F17F Mouse 10kb plasmid clone UUGC2M0258F17 F, genomic
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3-1 Yamada-oka, S
                                                       plasmid inserts
                                                                                                                                                                                                                                                  Mus musculus
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GSS.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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EST.
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                                       Unpublished (2000)
                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_Type="mRNA"
/mol_Type="mRNA"
/db xref="taxon:9606"
/clone="mp0338"
/clone= lib="Human promyelocyte"
/note="Female, adult, cell_line = HL60, cell_type
promyelocyte. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.8%;
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Pred. No. 3.5e+05;
                                                                                                                                                                                                                                                                                                                                              genomic survey sequence.
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                 Mouse whole genome scaffolding with plasmid inserts Unpublished (2000)
                                                                        Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                           1M0530D13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0530D13 R, genomic survey sequence.
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AZ655652.1 GI:11792798
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Fax: 801 585 7177
                                                                                                                                                                                                                                                  Mus musculus (house mouse)
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 Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.3%;
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Score 13.2; DB 9; Pred. No. 5.2e+05; D; Mismatches 3;

Length 22;

0

Gaps

0

24 bp

DNA

GSS 14-DEC-2000

paired end reads from 10kb

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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0258 row: F column: 17
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 22.
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Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lass: plasmid ends
musculus CSTBLI/GJ (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 0.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. coli strain XL10-Gold, T1-resistant, F
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="UUGC2M0258F17"
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FAX: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.
Plate: 0530 row: D column: 13
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                    1 (bases 1 to 28)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AA864650.1 GI:2958963
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28 bp mRNA linear EST 13-MAY-1998 oh37b09.s1 NCI CGAP Kid6 Homo sapiens cDNA clone IMAGE:1459961 3' similar to SW:ATPQ_BOVIN P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
                                            Unpublished (1997)
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                           Homo sapiens
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="UUGC1M0530D13"
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76.2%;
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Pred. No. 6.3e+05;
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Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 29)
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                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0336 row: J column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                       Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                           plasmid inserts
Unpublished (2000)
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                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                             Class: plasmid ends
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               quality sequence stop: 29
Location/Qualifiers
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/clone_lib="NCI_CGAP_Kid6"
/note="Cygan: kidney; Vector: Bluescript SK-; Site_1:
/note="Cygan: kidney; Vector: Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5'
CRANTCGCACGAG 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 6.
ive 0; Mismatches
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/mol\_type="genomic DNA" /strain="C57BL/6J"

organism="Mus musculus"

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2M0013A11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0013A11 F, genomic survey sequence
A2778032
                                                                                                                                                                                                                                                                                                                                                                                                 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Kose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0013 row: A column: 1
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Fax: 801 585 7177
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                 Class: plasmid ends
                                                                        Seq primer: CGTTGTAAAACGACGGCCAGT
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Location/Qualifiers
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Pred. No. 7.7e+05;
                                                                                                                       Std Error: 0.00
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                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: C
Plate: 0028 row: H column: 03
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                      plasmid inserts
Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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AZ785027.1 GI:12921357
GSS.
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                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                         University of Utah University of Utah
High quality sequence stop: 23
                        Class: plasmid ends
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                                                                                                                                                                                                                     Biomedical
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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CG730897/c
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CG730897
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                                                                                                                                       Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.

Reverse complemented post-ligation sequence from source sequence Plate: 1119130 row: F column: 05
                                                                                                                                                                                                                                   855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                               Maize genomic sequences 
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                           Stanford University
                                                                                                                                                                                                                                                                                                                                 Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                            Contact: Walbot
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/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background w23/A188/B73/K55"
                                                                                                   Location/Qualifiers
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/strain="C57BL/6J"
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78.9%;
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Pred. No. 9.2e+05;
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                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0118 row: G column: 01
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                          High
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
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                                                                                                                                                                                                                                                                           Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                            801 585 5606
801 585 7177
                                                                                                                                                                                                                                  quality sequence stop: 19.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="1119 - RescueMu Grid AA"
/clone lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.lastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
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/dev_stage="adult"
/lab_host="DH10B"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse_10kb_plasmid_UUGC1M_library"
/note="Vector: PWD42nv; Purified_genomic_DNA_from_M.
                                                                                                                                           /mol_type="genomic DNA"
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                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0138G01"
                                                                                                                                                                                        organism="Mus musculus"
                                                                           sex="Male"
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78.9%;
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UUGC1M library Mus musculus genomic
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SOURCE
ORGANISM
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AZ782026/c
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                                                                                                                                                                                                                                     Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0021 row: I column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ782026.1 GI:12915307
GSS.
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                                                                                                                                                                                                                                                                                                                                 Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 19)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (gi | 473214 | gb | ART29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
/lab_host="E. Coli strain XL10-Gold, T1-resistant,
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                     organism="Mus musculus"
                                                       sex="Male"
                                                                                   clone="UUGC2M0021I23"
                                                                                                             xref="taxon:10090"
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82.4%;
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Pred. No. 1.3e+06;
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UUGC1M library Mus musculus genomic
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KEYWORDS VERSION ACCESSION

FEATURES

FEATURES

'lab\_host="E. Coli strain XL10-Gold, T1-resistant,

COMMENT

COMMENT

TITLE

JOURNAL TITLE REFERENCE

AUTHORS

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Matches

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REFERENCE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0340 row: H column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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1 (bases 1 to 27)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ501699 27 bp DNA linear GSS 05-OCT-200 1M0340H12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0340H12 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                    /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                     clone="UUGC1M0340H12"
sex="Male"
                                                                                   db_xref="taxon:10090"
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SOURCE

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RESULT 13
AZ599021/c
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Best Local
                                                                                                                              Bource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0414 row: P column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid inserts
Unpublished (2000)
                                                                                                                                                Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                         308,
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                                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory Mouse DNA Resource
/db_xref="taxon:10090"
/clone="UUGC1M0414F08"
                                                                                                   organism="Mus musculus"
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Pred. No. 1.4e+06;
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AZ762096/c
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ORGANISM
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                                                                                                                source
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1M0556J18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0556J18 R, genomic survey sequence
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Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0556 row: J column: 18
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
Unpublished (2000)
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                                                                                                                                   High quality sequence stop: 24.
Location/Qualifiers
                                                                                                                                                                                      Class: plasmid ends
                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of phasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv; Purified genomic DNA from M.
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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Pred. No. 1.6e+06;
                                                                                                                                                                                                                                                                       Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                          20 S. 2030 E.,
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When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. GENOME SYSTEMS CLONE ID: Gm-c1005-102 Trace considered overall poor quality possible reversed clone: similarity on wrong strand This clone is available through: Biogenetic Services, 801 37nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Seq primer: T7 ET from Amersham High quality sequence stop: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khoema, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                           Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTCCCTCACCTCCAGCCACA 20
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EST.
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/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib-"Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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75.0%;
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RESULT 15 AI416870

DEFINITION

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Matches

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Search completed: March 25, 2006, 15:28:17 Job time : 3045.5 secs
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                                                                    CCCCCCCCCCCCACCCCCA
                                                                                                                                           Conservative
                                                                                                                                                                                                                               /clone lib="Gm-c1005"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; This library was constructed by Dr. Randy C.
Shoemaker and Dr. John Erpelding, USDA-ARS Agronomy
Department, G401 Agronomy Hall, Iowa State University,
Ames, IA 50011-1010 Phone: 515-294-6233 FAX: 515-294-2299
email: rcsshoe@iastate.edu"
                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/cullivar="Williams 82"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1005-102"
/lab_host="XL10-Gold"
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1

4: /cgn2_6/ptodata/1

5: /cgn2_6/ptodata/1

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Match
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301.980 Million cell updates/sec
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  ctccctcacctccagccacatg
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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ALIGNMENTS

#### CUMPULER: LEW COMPANDER: CLASSIFICATION NUMBER: COMPANDER: CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION UNMBER: SE9501324-9 FILING DATE: 10-APR-1995 PRIOR APPLICATION NUMBER: US08/522,595 FILING DATE: 01-SEP-1995 ATTORNEY/AGENT INFORMATION: NAME: Williams, Ph.D., Kathleen A REGISTRATION NUMBER: 34,380 REFERENCE/DOCKET NUMBER: 3255/5301: TELECOMMUNICATION INFORMATION: TELEPHONE: 617-345-9110 TELEPAX: 617-345-9111 INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: TENCTH: 24 bases RESULT 1 US-08-529-190B-16 US-08-529-190B-16 ; Sequence 16, ; Patent No. 5 GENERAL INFORMATION: TOPOLOGY: 11 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett COMPUTER: IBM Compat OPERATING SYSTEM: DO APPLICANT: MASUCCI, MARIA G. TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS CITY: Boston STATE: MA COUNTRY: USA TYPE: nucleic acid STRANDEDNESS: sing STREET: ADDRESSEE: 02111 5, Application US/08529190B 5833991 One Financial Center IBM Compatible linear Banner & Witcoff, Ltd. Diskette other nucleic acid 34,380 PR: 3255/53015

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TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
FILE REFERENCE: OHU-03417
CURRENT APPLICATION NUMBER: US/09/119,507B
CURRENT FILING DATE: 1998-07-20
NUMBER OF SEG ID NOS: 118
SOFTWARE: PATENTIN Ver. 2.0
SEG ID NO 38
LENGTH: 30
TYPES: NAS
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APPLICANT: Kieliszewski, Marcia J.
APPLICANT: Kieliszewski, Marcia J.
TITLE OF INVENTION: NO. 6548642el Synthetic Genes for Plant Gums
FILE REFERENCE: OHU-03417
CURRENT APPLICATION NUMBER: US/09/119,507B
CURRENT FILING DATE: 1998-07-20
NUMBER: OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 30
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Best Local S
Matches 17
                Sequence 10, Application US/08897556A Patent No. 6570062 GENERAL INFORMATION:
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Patent No. 6548642
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ORGANISM: Artificial Sequence
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 APPLICANT:
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FILLING DATE: 21-mm

CURRENT APPLICATION DATA: US/08/897 4277

FILLING DATE: 21-mm

CLASSIPPIA: 105/08/897 4277

CLASSIPPIA: 105/08/897 4277
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38, Application US/08897556A Patent No. 6570062
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,556A
FILING DATE: 21-UU-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 705-84
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OHU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               APPLICANT: KIELSZEWSKI, MARCIA J.
TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER
TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                    STATE: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid STRANDEDNESS: sing TOPOLOGY: unknown
                                                                                                                                                                                                                                                            CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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220 Montgomery Street,
                                                                                                                                                                                                                                                                           220 Montgomery Street,
                                                                                                                                                                                                                      United States of America
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Pred. No. 3.9e+03;
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t, Suite 2200
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REGISTRATION NUMBER:

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; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic
US-09-547-693-10
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US-09-547-693-10
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                                                   FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTMARE: PATENTIN VERSION 3.0
SEQ ID NO 38
LENGTH: 30
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOPTWARE: PatentIn version SEQ ID NO 10 LENGTH: 30 TYPE: DNA ORGANISM: Artificial/Unknown
                                                                                                                                                                                                                             Sequence 38, Application US/09547693
Patent No. 6639050
GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia
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Best Local Similarity
Matches 17; Conserv
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APPLICANT: Kielisz
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                                                                                                                                                                           TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich TITLE OF INVENTION: Glycoproteins FILE REFERENCE: OHU-04089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: OHU-04089
CURRENT APPLICATION NUMBER: US/09/547,693
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION: Synthetic Genes
TITLE OF INVENTION: Glycoproteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: (
                    ORGANISM: Artificial/Unknown FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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81.0%; Pred. No. 3.9e+03;
cive 0; Mismatches 4
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81.0%; Pred. No. 3
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                                                                                                                            US-08-529-190B-14
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US-08-529-190B-14/c
                                                            Query Match
Best Local Similarity
Matches 16; Conserv
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Patent No. 5
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                      TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE9501

PILING DATE: 10 APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US08/5

PILING DATE: 01-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: Williams, Ph.D., Kat

REGISTRATION NUMBER: 34,38
                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: Wordperfect 6.1 CURRENT APPLICATION DATA:
                                                                                                                                           TOPOLOGY: 1: MOLECULE TYPE:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Masucci, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 15-SEE CLASSIFICATION: 51
                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                      STRANDEDNESS: single
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5833991
CCCGCACCTCCAGCTCCAT 5
                              CCCTCACCTCCAGCCACAT 21
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                                                              Conservative
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GLYCINE-CONTAINING SEQUENCES
CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
                                                            64.5%; Score 14.2; DB 2;
84.2%; Pred. No. 5.6e+03;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                        US08/522,595
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Pred. No. 3.9e+03;
0; Mismatches 4
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RESULT 9 US-07-792-600-8

Sequence 8, Application US/07792600 Patent No. 6008045 GENERAL INFORMATION:

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                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence:
US-09-157-021-8
                                                                                                                                                                                                                                                                            APPLICANT: Copeland, William C.
APPLICANT: Wang, Teresa S. F.
TITLE OF INVENTION: Drug Design Assay
FILE REFERENCE: SIDU-03484
CURRENT APPLICATION NUMBER: US/09/157,021A
CURRENT FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: 07/792,600
EARLIER FILING DATE: 1991-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-09-157-021-8
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ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: STDU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 35
SOFTWARE: PATENTIN VER. 2.0
SEQ ID NO 8
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 0, Application US/09157021A Patent No. 6100023 GENERAL INFORMATION:
                                   Query Match
Best Local Similarity
Matches 16; Conserv
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/792,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Peter G. Carroll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: TEMPLATE-DEPENDENT ENZYMATIC SYNTHESIS OF NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 24 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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4 CCTCACCTCCAGCCACATG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220 Montgomery Street, Suite 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WANG, TERESA S.-F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COPELAND, WILLIAM C.
                                     Conservative
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                                                    64.5%;
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                                   0; Mismatches
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                                                      Score 14.2; DB 3
Pred. No. 5.6e+03
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Pred. No. 5.6e+03;
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                                                                          DB 3;
                                                                      Length 24;
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                                     Indels
                                                                                                                                 Synthetic
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; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER IMFORMATION: Description of Artificial Sequence: Synthetic US-09-156-842-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-156-842-8
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                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: US-09-591-514-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-591-514-8
                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Drug Design Assay
FILE REFERENCE: STDU-03484
CURRENT APPLICATION NUMBER: US/09/591,514
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: US/09/157,021
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 07/792,600
PRIOR FILING DATE: 1991-11-15
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 84.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Applic Patent No. 6103473
                                                                  Matches
                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 07/792,600 EARLIER FILING DATE: 1991-11-15 NUMBER OF SEQ ID NOS: 35 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: STDU-03485
CURRENT APPLICATION NUMBER: US/09/156,842A
CURRENT FILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Copeland, William C.
APPLICANT: Wang, Teresa S. F.
TITLE OF INVENTION: Drug Screening
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Copeland, William C. APPLICANT: Wang, Teresa S. F.
                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                    Local Similarity
                              4 CCTCACCTCCAGCCACATG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09591514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTCACCTCCAGCCAGGTG 19
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                                                                    Conservative
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                                                                                  64.5%;
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                                                                                  Score 14.2; DB 3
Pred. No. 5.6e+03
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Pred. No. 5.6e+03
0; Mismatches :
19
                                                                    Mismatches
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                                                                                                   Length 24;
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RESULT 13 US-09-887-145-6/c

; Sequence 6, Application US/09887145

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US-09-674-824-5/c

; Sequence 5, Application US/09674824

; Patent No. 6890732

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear;
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MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-887-145-6
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                              SEQ ID NO 5
-09-674-824-5
                                                                                                                                                                                               APPLICANT: LOTZ, et al
TITLE OF INVENTION: WUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT
TITLE OF INVENTION: WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH
FILE REFERENCE: AGR 1998/M 205/ FLH514413-3848
CURRENT APPLICATION NUMBER: US/09/674,824
CURRENT FILING DATE: 2000-02-16
PRIOR APPLICATION NUMBER: PCT/EP99/03156
PRIOR FILING DATE: 1999-05-07
PRIOR PILING DATE: 1998-05-08
PRIOR FILING DATE: 1998-05-08
NUMBER: OF SEQ ID NOS: 6
                                                                                                                                                                                SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Atent No. 6780641
GENERAL INFORMATION:
APPLICANT: Kim, Seung U
TITLE OF INVENTION: Immortalized human microglia
cell and continuous cell line
          FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(20)
OTHER INFORMATION: primer
                                                                                           LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence, primer
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MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb
COMPUTER: Dell PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Microsoft Word version 97
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNABER: US/09/887,145
FILING DATE: 22-Jun-2001
CLASSIFICATION: Unknown
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: DAVId PRABHKEY, ESQ.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: UBC-002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 CACCCTCAACGCCATCAACATG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CTCCCTCACCTCCAGCCACATG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Magnolia
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: David Prashker, Esq. STREET: P.O. Box 5387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (978) 525-3794
N FOR SEQ ID NO: 6:
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Pred. No. 6.8e+03;
0; Mismatches 5
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Search completed: March 25, Job time: 130.5 secs
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                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/487,368A
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 240
SEQ ID NO 216
LENGTH: 20
TYPE: DNA
ORGANIAM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 15
                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                              Patent No. 6261840 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 216, Application US/09487368A
                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                         APPLICANT: Lex M. Cowse:
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANT:
FILE REFERENCE: RTS-009:
                                                                                                                                                                              OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                       Local
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                                                                                                             16;
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                                                                                                                         Similarity
                                                     CTGCCCCAGCACCAGCCACA 20
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                                                                                                             Conservative
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                                                                                                                       61.8%; Score 13.6; DB 3; 80.0%; Pred. No. 9.8e+03;
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            2006, 13:03:00
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Pred. No. 8.1e+03;
0; Mismatches 2;
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                                                                                                                                    Length 20;
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Result
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Maximum Match
Listing first
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM nucleic - nucleic search, using sw model
   Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                       Score
   seq length:
seq length:
                                                                                                                                                                                                                                                                                                                                                                   Published_Applications_NA_Main:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
   Query
Match Length
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Gapop 10.0 , Gapext 1.0
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45 gt
10 US-11-036-317-179644

US-11-036-317-250940

10 US-11-036-317-253919

10 US-11-036-317-368615

US-11-036-317-391184

10 US-11-036-317-391184

10 US-11-036-317-39120

US-10-215-112-12019

US-10-215-112-12019

US-10-215-112-12145

US-10-215-112-12145

US-10-215-112-12186

US-10-719-900-217186

US-10-719-900-217186

US-10-719-900-217186

US-10-719-906-317-32785

US-10-719-956-459914

US-10-719-956-459914

US-11-036-317-360952

US-11-036-317-360952
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US-10-798-652-7

US-10-719-900-693282

US-10-956-157-252303

US-10-485-048-86
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                               Sequence 579816,
Sequence 12019, A
Sequence 12145, A
Sequence 278200,
Sequence 386177,
Sequence 217185,
Sequence 217186,
Sequence 217186,
Sequence 132785,
Sequence 459914,
                                                                                                                                Sequence 6, Appli
Sequence 7, Appli
Sequence 693282,
Sequence 252303,
Sequence 179644,
Sequence 250940,
Sequence 250940,
Sequence 268615,
Sequence 362146,
Sequence 362146,
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Sequence 280075,
Sequence 360952,
Sequence 469308,
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US-10-798-652-6
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Matches 22
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14.2	14.2	14.2	14.2	14.2	14.2	14.2		14.6			14.6		14.6	14.6		14.6	14.6	14.6	14.6	14.6	14.6
	64.5		64.5					66.4	σ	66.4	σ	66.4	σ	g	66.4	S.	66.4	66.4	6	66.4	66.4
25	25	25	25	25	25	25	25	30	30	30	30	30	30	30	30	25	25	25	25	25	25
9	9	9	9	8	8	7	7	9	9	æ	80	Φ	σ	9	σ	10	10	10	10	10	10
US-10-956-157-70584	US-10-956-157-70583	US-10-956-157-70582	US-10-956-157-70581	US-10-719-900-693283	US-10-719-900-221421	US-10-681-773-98599	US-10-681-773-98598	US-10-418-032-38	US-10-418-032-10	US-10-257-199-38	US-10-257-199-10	US-10-395-402-38	US-10-395-402-10	US-10-437-708-38	US-10-437-708-10	US-11-060-756-20618	US-11-060-756-20600	US-11-036-317-980808	US-11-036-317-927798	US-11-036-317-897472	US-11-036-317-516411
70584,	Sequence 70583, A	Sequence 70582, A	Sequence 70581, A	Sequence 693283,	Sequence 221421,	Sequence 98599, A	9859	38,	-	θ,	Sequence 10, Appl	Sequence 38, Appl	10,	38,	$\mathbf{r}$	20618,	Sequence 20600, A	Sequence 980808,		Sequence 897472,	Sequence 516411,

# ALIGNMENTS

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Sequence 6, Application US/10798652

Publication No. US20040219582A1

GENERAL INFORMATION:
APPLICANT: Yongjun Guo
ITITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISM IN THE
ITITLE OF INVENTION: FGF-3 GENE AND METHODS OF USE THEREOF
FILE REFERENCE: 3382-P03116US01

CURRENT APPLICATION NUMBER: US/10/798,652

CURRENT FILING DATE: 2004-03-11

PRIOR APPLICATION NUMBER: 60/455,698

PRIOR APPLICATION NUMBER: 60/455,698

PRIOR APPLICATION NUMBER: 60/455,698

PRIOR FILING DATE: 2003-03-17

SOPTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 6

LENGTH: 22

TYPE: DNA

CORANTSM. Artificial Screens
                                                                 RESULT 2
US-10-798-652-7
(Sequence 7, Application US/10798652
; Publication No. US20040219582A1
; GENERAL INFORMATION:
   APPLICANT: Yongjun Guo
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISM IN THE
   TITLE OF INVENTION: FGF-3 GENE AND METHODS OF USE THEREOF
   FILE REFERENCE: 3382-PO3136US01
; CURRENT APPLICATION NUMBER: US/10/798,652
; CURRENT FILING DATE: 2004-03-11
; CURRENT FILING DATE: 2004-03-11
PRIOR APPLICATION NUMBER: 60/455,698 PRIOR FILING DATE: 2003-03-17 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 22; DB 100.0%; Pred. No. 11;
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US-10-56-157-252303/c
US-10-956-157-252303/c
; Sequence 252303, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-693282
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                                                                                                                ; ORGANISM: Probe Sequence US-10-956-157-252303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 693282
                                              Query Match
Best Local Similarity
Matches 17; Conserv
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SEQ ID NO 7
                                                                                                                                                                             SEQ ID NO 252303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                     APPLICANT: MOUNTS, WILLIAM
TITLE OF INVENTION: NUCLRIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: 031896-043000 (AM 101081)
CURRENT FOLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SOFTWARE: Patentin version 3.2
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                               TYPE: DNA
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CTCCCTCACCTCCAGCCAC 19
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89.5%;
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89.5%;
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Pred. No. 53
                                                                Score 15.8;
Pred. No. 4.
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Pred. No. 4.6e+03;
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. 4.6e+03;
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                  RESULT 7
US-11-036-317-250940
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 Sequence 250940, Application US/11036317
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RESULT 5
US-10-485-048-86/c
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US-11-036-317-179644/c
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                                                                          Query Match
Best Local S
Matches 18
                                                                                                                                                                                          APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 179644
LENGTH: 25
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 86
LENGTH: 25
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CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: PCT/EP02/08343
PRIOR FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: GB 0118367.2
PRIOR FILING DATE: 2001-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Vaccine Comprising GP120 and NEF and/or TITLE OF INVENTION: TAT for the Immunisation Against HIV FILE REFERENCE: B45279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ERTL, Peter Franz
APPLICANT: TITE, John Philip
APPLICANT: VAN WELY, Catherine Anne
APPLICANT: VOSS, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Williams, Alan APPLICANT: Blume, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: primer (Figure 21)
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23
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                                                                          18; Conservative
                                    1 CTCCCTCACCTCCAGCCACATG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTCCCTCACCTCCAGCCACATG 22
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  CCCACTCCCCTCCAGCCACAGG
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                                                                                            70.9%;
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                                                                          Score 15.6; DB 10
Pred. No. 5.6e+03;
0; Mismatches 4
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                                                                            Indels
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US-11-036-317-253919
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, Sequence 253919, Application US/11036317
, Publication No. US20050214823A1
, GENERAL INFORMATION:
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CURRENT FILMG DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US/11/036,317
CURRENT FILMG DATE: 2005-01-13
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 250940
LENGTH: 25
TYPE: DNA
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 268615
                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                            Sequence 268615, Application US/11036317 Publication No. US20050214823A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 253919
LENGTH: 25
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Best Local Similarity 81.8%;
                                                    APPLICANT: Williams, Alan
APPLICANT: Williams, Alan
APPLICANT: Blume, John
ITILE OF INVENTION: Method of Analysis of Alternative Splicing
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Williams, Alan APPLICANT: Blume, John
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APPLICANT: Blume, John
APPLICANT: NUMENTION: Method of Analysis of Alternative Splicing in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication No. US20050214823A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 991174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Similarity 81.8%;
18; Conservative
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Pred. No. 5.
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Pred. No. 5.6e+03
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; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Se
; SEQ ID NO 391184
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-391184
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                                                                                                                                                                                                          GREERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Williams, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT APPLICATION NUMBER: US/60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PRIOR TILING DATE: 2004-01-13
                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                   Sequence 391184, Application US/11036317
Publication No. US20050214823A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 362146
                                  Matches
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Best Local
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Best Local Similarity
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APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION STATE OF SEQ ID NOS: 991174
NUMBER OF SEQ ID NOS: 991174
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Similarity 81.8%;
18; Conservative
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 CTCCCTCACCTCCAGCCACATG 22
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                               Score 15.6; D
Pred. No. 5.6e
0; Mismatches
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Pred. No. 5.6e+03;
0; Mismatches 4
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Pred. No. 5.6e+03;
0; Mismatches 4
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                                                .6e+03;
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RESULT 14
US-10-215-112-12145
Sequence 12145, Application US/10215112
Publication No. US20030082596A1
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
TITLE OF INVENTION: Method of Genetic Analys
TITLE OF INVENTION: Test3
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
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US-11-036-317-579816/c
US-11-036-317-579816/c
Sequence 579816, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
   APPLICANT: Williams, Alan
; APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
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US-10-215-112-12019
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CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FRANCEQ for Windows Version 4.0
SEQ ID NO 12019
LENGTH: 25
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 579816
LENGTH: 25
TYPE: DNA
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Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
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TITLE OF INVENTION: Method of Genetic Analysis
TITLE OF INVENTION: Test3
FILE REFERENCE: 3119
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                                                                                                   of Genetic Analysis
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Pred. No. 6.8e+03;
0; Mismatches 1
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Pred. No. 8.3e+03
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; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-278200
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FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12145
Search completed: March 25, Job time: 661.5 secs
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US-11-036-317-278200/c
; Sequence 278200, Application US/11036317
; Publication No. US20050214823A1
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APPLICANT: Williams, Alan
APPLICANT: Blume, John
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
CURRENT APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
PRIOR FILING DATE: 2004-01-13
PRIOR FILING DATE: 2005-01-14
                                                                                                                                                                                                                                                    SOFTWARE: Microarray Probe Sequence Listing Generator SEQ ID NO 278200 LENGTH: 25
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SEQ ID NO 12145
LENGTH: 25
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Local Similarity 85.0%;
les 17; Conservation
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Pred. No. 8.3e+03;
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Pred. No. 8.3e+03
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Perfect score:
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| SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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| SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
| SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
| SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
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  WS-10-310-914A-613434

WS-10-310-914A-233742

WS-10-310-914A-117759

WS-10-310-914A-91863

WS-10-310-914A-91863

WS-10-310-914A-91863

WS-10-310-914A-91863

WS-10-310-914A-448406

WS-10-310-914A-1002544

WS-10-310-914A-1002544

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Biocceleration
Sequence 448407,
Sequence 1002544,
Sequence 180307,
Sequence 66290, A
Sequence 196424,
Sequence 196424,
Sequence 228828,
Sequence 228828,
Sequence 66277, A
                                                                                                                                                                                                                                    Sequence 613434,
Sequence 233742,
Sequence 668834,
Sequence 317759,
Sequence 377554,
Sequence 91862, A
Sequence 91863, A
Sequence 91863, A
Sequence 724597,
Sequence 724597,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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APPLICANT: Shiler, Kvuzat
FIITE OF INVENTION: Bioinformatically detectable group of
FITTLE OF INVENTION: Bioinformatically detectable group of
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 613434
FINGANISM: Human
ORGANISM: Human
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## ALIGNMENTS

of novel regulatory genes

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US-10-310-914A-233742

Sequence 233742, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
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Best Local S
Matches 15
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
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; ORGANISM: Human
US-10-310-914A-233742
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Best Local Similarity
"hehes 17; Conserv
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US-10-310-914A-668834/c
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Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiber, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087,0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 233742
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 668834
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Best Local Similarity
Matches 16; Conserv
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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Pred. No. 8.9e+02;
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Pred. No. 1.
                                                                                  Score 16.4; DB 8;
Pred. No. 1.3e+03;
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes (
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 377554
LENGTH: 20
TYPE: RNA
ORGANISM: Human
US-10-310-914A-377554
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US-10-310-914A-377554/c
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 91862
LENGTH: 25
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of
TITLE OF INVENTION: uses thereof
TITLE OF INVENTION: 06087.0200.CPUS01
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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Best Local Similarity
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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85.7%;
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Pred. No. 1.
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Pred. No. 1.3e+03;
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; Sequence 724597, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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                                                                                                                                                                       TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and TITLE OF INVENTION: uses thereof FILE REFERENCE: 06087.0200.CPUS01 CURRENT APPLICATION NUMBER: US/10/310,914A CURRENT FILING DATE: 2002-12-06 NUMBER OF SEQ ID NOS: 1388402 SOFTWARE: PatentIn version 3.3 SEQ ID NO 724597 LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Shiler, Kouzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TILE REFERENCE: 06087 0200. CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 488406
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Publication No. US20060003322A1
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                                                                                                                                            TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
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                                                                            71.8%;
89.5%;
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78.9%;
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85.7%; Pred. No. 1
                                                           Score 15.8; D
Pred. No. 2.3e
0; Mismatches
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2.3e+03;
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                                                                                                                                                         Sequence 180307, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEO ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEO ID NO 448407
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Best Local Similarity
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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Best Local (
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
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ORGANISM: Human
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TYPE: RNA
ORGANISM: Human
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; Pred. No. 2.4e
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Pred. No. 2.4e+(
2; Mismatches
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CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: PRODRIEGATY
SEQ ID NO 196424
LENGTH: 19
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                                                     ; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-196424
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
TITLE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 66290
LENGTH: 24
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Query Match
Best Local Similarity
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Best Local (
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Best Local Similarity
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APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
FILE REFERENCE: 13499US
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APPLICANT: Khvorova,
APPLICANT: Reynolds,
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ORGANISM: Human
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ORGANISM: Human
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Reynolds, Angela
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89.5%; Pred. No. 2.
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70.0%;
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Pred. No. 2.9e+03;
2; Mismatches 4
 Score 15.4; DB 12;
Pred. No. 3.4e+03;
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Search completed: March 25, 2006, 14:54:04 Job time: 315.5 secs
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US-11-083-784-196424
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US-11-083-784-196424/c
; Sequence 196424, Application US/11083784
; Publication No. US20050245475A1
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CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR PILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR PILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR PILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
                                                                                                                                             Query Match
Best Local Similarity
Matches 16; Conserv
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APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional sirNA
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                                                                                                                                                                                                                                                        TYPE: RNA
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Reynolds, Angela
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Pred. No. 3.4e+03;
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Match
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Gapop 10.0 , Gapext 1.0
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AX501648	AX501647	AX501646	AX501645	AX501644	BD185138	BD174183	AX290630	AR442798	AR105954	AR096578	AR052983	A57536	A57517	AX033501	BD249866	CS095413	CS095314	AX817728	CS012518	BD185155	BD174200	AX598365	AR379426	AR412132	AR412123	AR340063
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### ALIGNMENTS

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SOURCE REFERENCE AUTHORS TITLE 밁 S FEATURES source Query Match Best Local S Matches 16 JOURNAL 11 16; AX701087 Sequence 86 from Patent AX701087 AX701087.1 GI:29536869 4 CCTCGCCTCCAGCCACATG unclassified sequences.

1 (bases 1 to 30)

1 (rie, R.F. and Kikumotto, Y.

TUMOR ASSOCIATED POLYPEPTIDES WITH CARBOXYL-TERMINAL
TUMOR ASSOCIATED POLYPEPTIDES WITH CARBOXYL-TERMINAL 30 bp Sequence 3 from Patent WO9714795 A79795 synthetic construct Patent: WO 9714795-A 3 24-APR-1997; WAYNE JOHN CANCER INST (US) ALANINE-PROLINE, PROLINE-PROLINE OR GLYCINE-PROLINE AND ANTIBODIES unidentified unidentified A79795.1 THERETO Similarity ccececcrccaecrccare 29 Conservative /organism="unidentified" /mol\_type="unassigned DNA" /db\_xref="taxon:32644" Location/Qualifiers
1. .30 GI:6092713 25 bp from Patent WO03011334. 64.5%; Score 14.2; DB Pred. No. 1.4e+0; Mismatches 22 DB 6; .4e+05; les 3; DNA DNA Length 30; linear linear PAT PAT 0 03-APR-2003 20-OCT-1999 Gaps 0

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Patent: WO 03011334-A 86 13-FEB-2003;
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Sequence 956 from Paten
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AX444501.1 GI:21691779
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Department of Health and Human Services (US)
Location/Qualifiers
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Sequence 7 from Patent WO2005052140.
CS109308 GI:68148122
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Gunderson, K.
Probes and decoder oligonucleotides
Patent: WO 0216649-A 956 28-FEB-2002;
                                                    synthetic construct synthetic construct other sequences; artificial sequences.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/mol_type="unassigned DN:
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                             62.7%;
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Pred. No. 2.1e+05;
0; Mismatches 2;
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Best Local Similarity 88.2%;
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PN JP 2001525168-A/21
PD 11-DEC-2001
PF 27-NOV-1998 JP 2000523326
PF 27-NOV-1997 GB 9725311.6,28-NOV-1997 GB 97253
PR 28-NOV-1997 GB 9725311.6,28-NOV-1998 GB 9824275.3
SANBING SHEN, ANDREAS SCHEDL, ANTHONY JOHN HARMAR PC
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1 (bases 1 to 22)
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  Schedl, A. and Harmar, A.J.
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Location/Qualifiers
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon;32630"
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/mol_type="unassigned DNA"
/mol_type="taxon:35630"
/moEe="Computer Generated Probe
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 ch 61.8%;
l Similarity 80.0%;
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WOO, S. L.C., Smith, L.C., Cristiano, R.J., Gott
Nucleic acid transporter system and methods
Patent: US 5994109-A 22 30-NOV-1999;
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Woo,S.L.C., Smith,L.C., Cristiano,R.J., Gottchalk,S.
Nucleic acid transporter system and methods of use
Patent: US 5994109-A 19 30-NOV-1999;
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ANDREAS (DE); HARMAR ANTHONY
Location/Qualifiers
                                                                                                                                                                                                   22
                                                 /organism="unknown"
/mol_type="unassigned
                                                                                                                                                                                                                                                                                                                                                          /organism="unknown"
/mol_type="unassigned DNA"
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/db xref="taxon:32630"
/noTe="Primer"
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Score 13.6; DB 6;
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AR125632/c
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WOO, S. L.C., Smith, L.C., Cristiano, R.J.,
Nucleic acid transporter systems
Patent: US 6177554-A 22 23-JAN-2001;
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l Similarity 80.0%;
16; Conservative
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Woo, S. L.C., Smith, L.C., Cristiano, R.J.,
Nucleic acid transporter systems
Patent: US 6177554-A 19 23-JAN-2001;
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          Homo sapiens
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/mol_type="unassigned
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Metazoa; Chordata;
                                       GI:30511867
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Sequence 10 from patent US
AR073296
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Sequences involved in phenomena of tumour suppression, tumour suppression, apoptosis and/or virus resistance and their use
                      IMMUNE-EVADING PROTEINS
Patent: WO 9632483-A 10 17-OCT-1996;
MASUCCI MARIA GRAZIA (SE)
Other publication AU 5284296 961030.
Location/Qualifiers
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Sequence 10 from Patent WO9632483.
A57518 GI:3713376
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Location/Qualifiers
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Conservative 0;
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/mol_type="unassigned DNA"
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/mol_type="unassigned
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                                                                                                                                                                                                                                                       synthetic construct synthetic construct other sequences, artificial sequences.
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Masucci, M.G.
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Patent: US 5833991-A 16 10-NOV-1998;
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/mol_type="unassigned DNA"
/mol_type="taxon:32630"
/mole="probe"
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Pred. No. 4.8e+05;
0; Mismatches 5
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Pred. No. 4.8e+05;
                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                   25 bp DNA
WO2004065583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 bp
5833991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invisibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 24;
                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 24;
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PAT 04-OCT-2004

0

Gaps

0

0

Gaps

0

밁 ঠ 밁 8

Search completed: March 25, 2006, 14:43:30 Job time: 960 secs

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Run
                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                              Database
                                                                                                                                                                                                                                                                                                                          Minimum DB
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                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                        seq length: 0 seq length: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic search, using sw model
 N_Geneseq_21:*
1: geneseqn1980
2: geneseqn2990
3: geneseqn2001
5: geneseqn2001
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9: geneseqn2003
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13: geneseqn2000
14: geneseqn2000
                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           March 25, 2006, 13:22:55; Search time 372.5 Seconds
(without alignments)
393.619 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                   4996997 segs, 3332346308 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-798-652-7
22
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geneseqn1990s:*
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                                                                                                                                                                                                              geneseqn1980s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Result No. Score	Query Match L	Length [	13 B	ID ADT97907
•	2 20.4	92.7	22	13	ADT97906
	3 15.4	70.0	20	14	AEA51146
	4 14.8	67.3	20	12	ADM79585
ი	5 14.6	66.4	29	14	ADY00944
	6 14.2	64.5	30	N	AAT90350
ი	7 14	63.6	25	10	ADB67764
	8 13.8	62.7	20	14	AEA51123
n	9 13.8	62.7	24	σ	ABQ00949
بر		62.7	24	0	ABQ05868
c 11	13	62.7	24	0	ABQ05827
12		61.8	20	4	AAS07411
13	3 13.6	61.8	22	ຎ	AAX57861
14		61.8	22	ഗ	AAC85242
0 1		61.8	25	φ	ACI88529
بر		01	25	9	ACH62883
<u> </u>	Lu.	01.0	25	9	ACH63009
င 1	7 13.6	61.8	27	w	AAA36652
c 1	13.6	61.8		•	

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13	13	13	13	13	13	13	13	13	13	13	13	13.2	13.2	13.2	13.2	13.2	13.2	13.2	13.2	13.6	13.6	13.6	13.6		
59.1	59.1	59.1	59.1	59.1	59.1	59.1	59.1	59.1	59.1	59.1	59.1	60.0	60.0	60.0	60.0	60.0	60.0	60.0	60.0	61.8	61.8	61.8	61.8	61.8	01.0
26	26	25	24	24	23	23	22	22	20	20	17	26	26	25	22	21	20	19	19	27	27	27	27	27	12
13	4	13	თ	N	14	N	13	10	14	13	œ	14	σ	N	10	σ	w	10	10	4.	4	4	4.	w	U
ADV69164	ABL41661	ADR00162	ABZ21805	AAV55821	ADV78737	AAZ09311	ADR88302	ADC36189	AEC02351	ADR87437	ABT38521	ADY49468	AAD46882	AAX25239	ADD22516	ABS98432	AAA53034	ADG34895	ADG35018	AAS08482	AAS08479	AAC82872	AAC82869	AAZ39499	770707
Adv69164 Human per	Abl41661 Primer #2	Adr00162 DAPK1 pro	Abz21805 PCR prime	Aav55821 Multimeri	Adv78737 PCR prime	Aaz09311 Human mac	Adr88302 Mus muscu	Adc36189 Weed cont	Aec02351 Stokesia	Adr87437 Epoxygena	Abt38521 Tumour su	Ady49468 Human neu	Aad46882 Probe H1P	Aax25239 Maize cin	Add22516 Flatfish	Abs98432 Human mul	Aaa53034 Human cDN	Adg34895 Human TNF	Adg35018 Human TNF	Aas08482 DNA ligan	Aas08479 C-myc DNA	Aac82872 Nucleic a	Aac82869 Nucleic a	Aaz39499 C-myc pro	Parantae series

# ALIGNMENTS

RESULT 1 ADT97907

ADT97907 standard; DNA; 22 BP.

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Human; ss; fibroblast growth factor-3; FGF-3; cancer; oesophageal cancer; breast cancer; ovarian cancer; prostate cancer; head and neck cancer; oesophageal squamous cell carcinoma; PCR; probe; SNP; single nucleotide polymorphism.
                    Guo Y;
                                                          17-MAR-2003; 2003US-0455689P
                                                                                                   04-NOV-2004.
                                                                                                                                                                                                                                 modified_base
                                                                                                                                                                                                                                                                                                                                     Human FGF-3 promoter 5' proximal region C allele probe.
WPI; 2004-794435/78.
                                                                              11-MAR-2004; 2004US-00798652
                                                                                                                       US2004219582-A1.
                                                                                                                                                                               modified_base
                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                           27-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                               ADT97907;
                                        (GUOY/)
                                        GUO
                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                /*tag= a
/mod_base= OTHER
/note= "C is covalently linked to a 6-carbo fluorescein
moiety (FAM)"
                                                                                                                                     /*tag= b
/mod_base= OTHER
/mod_base= OTHER
/note= "G is covalently linked to a TAWRA moiety (6-
carbotetramethyl-rhodamine)"
                                                                                                                                                                                                                                      Location/Qualifiers
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RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC vector, detecting a SNP in the FGF-3 gene in a mammal (involves isolating CC a nucleic acid sample from the mammal, and determining whether a cytosine CC or thymine is present at position 69 ofADT97901), a kit for performing CC the method (comprising a first oligonucleotide probe which anneals CC specifically with the target portion of the mammal's genome, where the CC first probe comprises a first fluorescent label and a first fluorescence CC quencher attached to its separate nucleotide residues and the target CC portion includes the nucleotide residue located at position 69 of ADT97901, and a pair of primers for amplifying a reference portion of the CC ADT97901, and a pair of primers for amplifying a reference portion of the CC GC gene, where the reference portion includes the nucleotide residue located at position 69 of ADT97901) and a microarray having at least one oligonucleotide probe that can anneal with a target portion of a mammal's CC genome, where the target portion includes the nucleotide residue located CC stocked at position 69 of ADT97901. The method is useful for detecting SNP in FGF CC genome, where the target portion includes the nucleotide residue located CC at position 69 of ADT97901. The method is useful for assessing CC the relative susceptibility of a mammal to cancer (especially ossophageal CC cancer), which shows an association with the presence of the C-allele. CC The cancer is chosen from ossophageal cancer is ossophageal squamous cell carcinoma. The present sequence is a fagman PCR probe used to genotype in the UTR of FGF-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      upstream untranslated region (UTR) of fibroblast growth factor (FGF) -3 gene sequence (ADT97901) with a single nucleotide polymorphism (SNP) at position 69. Also included are an isolated nucleic acid molecule comprising a sequence complementary to ADT97901, a vector comprising the ADT97901 operably linked to a reporter gene, a host cell comprising the vector, detecting a SNP in the FGF-3 gene in amammal (involves isolating a nucleic acid sample from the mammal and determine the comprision and contract acid sample from the mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule having single nucleotide polymorphism in upstream untranslated region of fibroblast growth factorgene, useful for assessing related susceptibility of mammal to cancer.
                                                                                                                                     modified_base
                                                                                                                                                                                                                                                                          Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ss; fibroblast growth factor-3; FGF-3; cancer; oesophageal cancer; breast cancer; ovarian cancer; prostate cancer; head and neck cancer; oesophageal squamous cell carcinoma; PCR; probe; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human FGF-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADT97906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADT97906 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 7; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                individuals for the C SNP
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22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCCTCGCCTCCAGCCACATG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter 5' proximal region T allele probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
(larity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
/mod_base= OTHER
/note= "G is covalently linked to a TAMRA moiety (6-
carbotetramethyl-rhodamine)"
                                                                                                                                                                                                                      /*tag=
/mod_ba
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                              *tag= b
                                                                                                                                                                                 note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymorphism.
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                                                                                                                                                                             base= OTHER
e= "modified with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the UTR of FGF-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                             Vic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,
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Unidentified

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AEA51146
ID AEA5
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AC AEA5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC comprising a sequence complementary to ADT97901, a vector comprising a SNP in the FGF-3 gene in a mammal (involves isolating CC ADT97901 operably linked to a reporter gene, a host cell comprising the CC vector, detecting a SNP in the FGF-3 gene in a mammal (involves isolating CC a nucleic acid sample from the mammal, and determining whether a cytosine CC or thymine is present at position 69 ofADT97901), a kit for performing CC the method (comprising a first oligonucleotide probe which anneals CC generic ally with the target portion of the mammal's genome, where the first fluorescent label and a first fluorescence CC quencher attached to its separate nucleotide residues and the target CC portion includes the nucleotide residue located at position 69 of ADT97901, and a pair of primers for amplifying a reference portion of the CC ADT97901, and a pair of primers for amplifying a reference portion of the CC alpman, where the reference portion includes the nucleotide residue CC enome, where the target portion includes the nucleotide residue CC at position 69 of ADT97901. The method is useful for detecting SNP in FGF CC annear in a mammal, preferably a human, and is also useful for assessing the relative susceptibility of a mammal to cancer (sepecially ossphageal CC and neck cancer. The ossphageal cancer is cosephageal squamous cell cc carcinoma. The present sequence is a Tagman PCR probe used to genotype individuals for the T SNP in the UTR of FGF-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                upstream untranslated region (UTR) of fibroblast growth factor (FGF)-3 gene sequence (ADT97901) with a single nucleotide polymorphism (SNP)at position 69. Also included are an isolated nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-NOV-2004
                                                              Expression; protein production; selectable marker; ss; pyrF; PCR; primer
                                                                                                                                pyranalR primer,
                                                                                                                                                                                                   11-AUG-2005
                                                                                                                                                                                                                                                              AEA51146;
                                                                                                                                                                                                                                                                                                                             AEA51146 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid molecule comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 34; SEQ ID NO 6; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-794435/78.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                               (first entry)
                                                                                                                                SEQ ID NO: 20 to construct pyrF selection marker system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.7%;
95.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20.4;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth factor-
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RESULT 4
ADM79585
ID ADM7
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides an improved expression system for the production of recombinant polypeptides utilizing auxotrophic Pseudomonas cell selectable markers. The invention also provides improved recombinant protein production in host cells through improved regulation of expression. The present sequence is the PCR primer used to construct pyrf selection marker system in a Pseudomonas fluorescens host cell expression
                                                                                                                                                                                tumour suppressor; chromosome 13; cytostatic; abnormal cell proliferation inhibitor; caspas mutation; detection; PCR; primer; ss.
                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New auxotrophic Pseudomonad cell for use in a bacterial expression system that comprises a nucleic acid construct encoding a polypeptide that restores prototrophy to the host cell, useful for producing of
WPI; 2004-330451/30.
                                                                                                                              WO2004033659-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-NOV-2003; 2003US-0523420P
16-JAN-2004; 2004US-0537147P
                                                                                   10-OCT-2003;
                                                                                                        22-APR-2004.
                                                                                                                                                                                                                                                                                                    ADM79585
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-417995/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schneider JC,
                                          (UYJE-) UNIV
                                                                                                                                                                                                                                                           15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-NOV-2004; 2004WO-US038884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2005052151-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DOMC )
                                                                                                                                                             sapiens
                                                                                                                                                                                                                                  ARTS1 related G446A mutation detection primer
                                                                                                                                                                                                                ARTS1;
                                                                                                                                                                                                                                                                                                                                                          _
                                                                                                                                                                                                                                                                                                                                                                              S
                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOW GLOBAL
                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                       CTCGCCTCCAGCCACAT 21
                                                                                                                                                                                                                                                                                                                                                       CTCGCCTCCTGCCACAT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                            ₿P;
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                   2003WO-US032270.
                                          JEFFERSON THOMAS
                                                              2002US-0417842P.
                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                               ADP-ribosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID NO 20; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             4 A;
                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                            70.0%;
94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                                                                                                                                                                            C; 2
                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Badgley AK,
                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                           G; 4
                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.4; DB 14; Pred. No. 7e+03;
                                                                                                                                                                                                             factor-like tumour suppressor 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INC
                                                                                                                                                                                                                                                                                                                                                                                                                                           т;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ramseier TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                           u; o
                                                                                                                                                                                          caspase-1 protease modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Other;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                   Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                        20,
                                                                                                                                                                                                                                    NO:14
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                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Sequence

20

BP; 4

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8 C; 4 G;

4 T; 0 U;

0 Other;

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an example from the present invention.

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CC nucleotides (3) a recombinant expression vector (IV) comprising (III);

(C) (4) a host cell comprising (IV); (5) an Oligonucleotide molecule (V)

(C) (4) a host cell comprising (IV); (5) an Oligonucleotide molecule (V)

(C) (4) a host cell comprising (IV); (5) an Oligonucleotide molecule (V)

(C) (4) a host cell comprising (IV); (5) an Oligonucleotide molecule (V)

(C) (4) a host cell comprising (IV); (5) an Oligonucleotide molecule (V)

(C) (4) a host cell comprising (IV); (5) an Oligonucleotide molecule (V)

(C) (4) a host cell comprising (IV); (5) an Oligonucleotide molecule (V)

(C) (4) a host cell comprising (IV); (6) an isolated antibody

(C) (4) a host cell comprising (IV); (6) an isolated antibody

(C) (4) a host cell complementary to a nucleotide sequence

(C) (VI) that binds to an epitope on SEQ ID NO:1. Human ARTS1 has cytostatic

(C) (VI) that binds to an epitope on SEQ ID NO:2; and (6) an isolated antibody

(C) (VI) that binds to an inhibitor of proliferation of the suseful for protein activity which involves performing a test caspase-1 protease

(C) caspase-1 protease protein with a caspase-1 substrate such as FKBP46

(C) protein in the presence of the test compound, determining the level of component of processing of a caspase-1 substrate by caspase-1 protease

(C) protein in the absence of the test compound, (I) and (II) are useful for protease protein in the absence of the test compound, (I) and (II) are useful for contenting abnormal cell growth in mammalian subjects. (II) is useful for contenting protein (V) is useful as a probe in oligonucleotide hybridisation content the detection of the AFCS. The present sequence represents a PCR content of the case of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel ADP-ribosylation factor-like tumor suppressor 1 (ARTS1) useful for identifying modulators of Caspase-1 protease protein and for preventing abnormal cell growth in mammalian subjects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes the human ARTS1 (ADP-ribosylation factor-
like tumour suppressor 1) protein (I). The human ARTS1 gene is located on
chromosome 13, more specifically to 13q14. Also described: (1) an
isolated nucleic acid molecule (II) comprising a sequence that encodes
(I), (2) an isolated nucleic acid molecule (III) comprising the 3791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 14; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein activity
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                                                                                                                                                                                                                                             RESULT 5
ADY00944/c
                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
                24-JUL-2003;
25-NOV-2003;
25-NOV-2003;
                                                                                                                                 gynecology and obstetrics; neoplasm; cytostatic; metastasis; gene therapy; RNA interference; UDP-galactose 4-epimerase; UDP-glucose 4-epimerase; lysophospholipase; HT014; LOC148902
                                                  27-MAY-2004; 2004WO-US016939
                                                                                       WO2005014846-A2
                                                                                                         Homo
                                                                                                                                                             SNP detection; breast tumor; endocrine disease;
                                                                                                                                                                              PCR primer 170 used to amplify human GALE
                                                                                                                                                                                                05-MAY-2005
                                                                                                                                                                                                                   ADY00944;
                                                                                                                                                                                                                                    ADY00944 standard; DNA;
(SEQU-) SEQUENOM INC
                                                                      17-FEB-2005.
                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                  v
                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                   CTCGCCTCCAGCCACATG
                                                                                                                                                                                                                                                                                 CTCGCCTGCAGACACATG
                ; 2003US-0490234P.
; 2003US-00723681.
; 2003US-0525239P.
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                 (first
                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                           67.3%;
                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                     ВP
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                                                                                                                                                                                                                                                                                                                            Score 14.8; DB 12
Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                     DB 12;
                                                                                                                                                                              region
                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                               SNP
                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                   LOC148902; LYPLA2;
                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                            GALE;
                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 6
AAT90350
ID AAT90350
ID AAT90350
AC AAT9
AC AAT9
XX DNA
XX DNA
XX Tuno
KW Tuno
KW Tino
CKW Tuno
CKW WPI;
CKW WP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention demonstrates cytostatic activity and may be useful for identifying a risk of, preventing and/or treating breast cancer and cancer metastasis. The methods may be utilized for gene therapy or interference. The current sequence is that of a PCR primer of the invention which was used to amplify a human HT014/LOC148902/LYPLA2 (lysophospholipase II)/GALE (galactose-4-epimerase, UDP-) DNA contains the property of the contains of the contai
                                                                                                                                                                                                                                                                              Antibody against polypeptide having C-terminal amino acid comprising Ala-Pro, Gly-Pro or Pro-Pro - useful to purify which can be useful in human melanoma treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-245112/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis; prognosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding peptide immunoreactive with HuMAb L94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT90350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT90350 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method for identifying a subject at risk of breast cancer comprising detecting the presence or absence of a polymorphic variation associated with breast cancer. The method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying risk of, preventing and/or treating breast identifying and/or analyzing polymorphic variations in sequences within the human genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-163257/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roth RB, Nelson MR,
Hoyal-Wrightson CR;
                                                                                                                                                                                        Example 1; Page 40; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Irie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-OCT-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour associated antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (WAYN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WAYNE CANCER INST JOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW26567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCTCTCTCCTCCCTCCACAT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCCTCGCCTCCAGCCACAT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kikumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 8 A; 1 C; 16 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 208; 617pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US013331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-US013331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.4%;
81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymorphism (SNP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Braun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanoma; cancer; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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Pred. No. 1.
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This nucleotide sequence codes for a immunoreactive with human monoclonal human melanoma cell line. It was obta

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peptide (see AAW26567) that is antibody JWCI L94 that reacts to ained by screening melanoma M14 ar

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RESULT 7
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The present invention describes the use of an HIV Tat protein or CC polynucleotide, an HIV Nef protein or polynucleotide, or an HIV Tat CC protein or polynucleotide linked to an HIV Nef protein or polynucleotide, or and an HIV Tat CC and an HIV Gp120 protein or polynucleotide in manufacturing a vaccine for CC a prime-boost delivery for the prophylactic or therapeutic immunisation CC of humans against HIV. The protein or polynucleotide is delivered via a CC bombardment approach. Also described: (1) a recombinant DNA molecule CC comprising a Nef and/or Tat and/or gp120 gene in a vector in which the CC gene of interest is inserted 3' to an enhanced HCMV IEI promoter; (2) CC particles, preferably gold particles, coated with recombinant DNA CC comprising at least two different vaccine compositions including: (a) a kit CC composition comprising particles coated with DNA encoding gp120 and nef CC and/or tat or nef-tat; and (b) a composition comprising gp120 and nef CC coated onto the particles. The HIV proteins or polynucleotides are used CC coated onto the particles. The HIV proteins or polynucleotides are used CC to produce vaccines having anti-HIV activity. The recombinant DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of an HIV Tat, Nef or gp120 protein or polynucleotide i manufacturing a vaccine for a prime-boost delivery for the or therapeutic immunization of humans against HIV.
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                                                                                                                                                                                                                                             The present invention relates to postnatal periodontal ligament stem cells (PDLSCs). The invention is useful for periodontal tissue regeneration, periodontal disease treatment and differentiation of the cells and methods of tissue cryopreservation. The invention is also useful in cell therapy and in medical therapy e.g. for treating trauma. The present sequence is the human class II bHLH protein scleraxis (SCX) gene specific primer. This sequence is used in the isolation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated periodontal ligament multipotent stem cell, useful generating periodontal tissue or cells in a subject to reduce or ameliorate trauma such as periodontal disease or physical injury care.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 7;
                                                                                                                                                                                 B₽;
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                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
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                                                                                                              62.7%;
88.2%;
                                                                                                                                                                               9 C; 3 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      62pp;
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Pred. No. 2.7e
0; Mismatches
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                                                                                                              Score 13.8;
Pred. No. 3.
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                                                                                        Indels
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ID ABQ009
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ABQ05868
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Best Local
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                                                                                                                                           Oligonucleotide
                                                                                                                                                                                        Oligonucleotide adapter/capture probe 5859
                                                                                                                                                                                                                                                                                                                                         ABQ05868 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Array comprising adapter sequences useful for immobilizing or detecting target nucleic acid sequence, has different addresses comprising
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                                             WO200216649-A2
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                                                                                                                                                                                                                                                                                           ABQ05868;
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29-AUG-2000;
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2000US-0228854P.
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                                                                                                                                           array; adapter sequence; probe;
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Pred. No. 3
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RESULT 11
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Best Local S
Matches 15
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                         Array comprising adapter sequences useful for immobilizing or detecting target nucleic acid sequence, has different addresses comprising different specific capture probes.
                                                                                                                                                                                                                                                                                                             Oligonucleotide array; adapter sequence; probe; ss
                                                                                                                                                                                                                                                                                                                                      Oligonucleotide adapter/capture probe 5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24 BP; 7 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
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29-AUG-2000; 2000US-0228854P.
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                                                                                                          Gunderson
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29-AUG-2000; 2000US-0228854P.
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                                                                                                                                    (ILLU-) ILLUMINA INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCGCGTCCAGACACAT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                  entry)
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Pred. No. 3.2e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
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Claim 1; Page 161; 261pp; English

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RESULT 12
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ID AASO7411
XX AASO7411
XX AASO7411
AC AASO7
XX PCR F
XX Revol
KW Revol
KW PART
XX 
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Best Local S
Matches 15
                                                                                                                                                         AASO7401-AASO7571 represent REVOLUTA (REV) coding sequences and PCR primers of the invention. The REV nucleic acid sequences were isolated from plants such as Arabidopsis thaliana, tomato, corn, barley and rice. The REV gene is required to promote the growth of apical meristems, but has an opposite effect on mersitems of leaves, floral organs and stems, such that it acts to limit cell division reducing the rate of plant growth and final size of the tissue. Therefore, loss of functional REV leads to increases in the size of floral organs, leaf and stem tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a daspter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid for ma modified target nucleic acid and contacting the modified target nucleic acid which (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated protein,
                             DNA encoding the REV protein is useful for modulating plant cell division. The mutant REV DNA is also useful for producing transgenic plants with modulated cell division. These transgenic plants can be used to increase crop yield in cereals and fruits, and as a potential source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Revoluta; Rev; corn; barley; rice; tomato; PCR primer; apical meristem; leaf; floral organ; stem; transgenic plant; crop yield; cereal; fruit; pharmaceutical; industrial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Slade A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS07411 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24 BP; 5 A; 4 C; 8 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-328861/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-NOV-2000; 2000WO-US030794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200133944-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primer K21L19L used to map the REVOLUTA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS07411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 48; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SLAD/) SLADE A.
(MADI/) MADISEN L.
(COMA/) COMAI L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ຫ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA molecule comprising a sequence that encodes a REVOLUTA useful for producing transgenic plants with modulated cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCGCGTCCAGACACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCGCCTCCAGCCACAT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Madisen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0164587P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ហ
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Pred. No. 3.2e+04;
0; Mismatches 2;
   products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                     be used
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밁 S

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RESULT 13
AAX57861
ID AAX57
XX AAX57
XX AAX57
XX YAC;
XX YAC;
XX YAC;
XX YAC;
XX YAC;
XX GB233
XX GB233
XX GB233
XX GB233
XX O2-JI
XX O2-JI
XX O2-JI
XX New
PR 28-NC

                                            CC artificial chromosome of the invention. The yeast artificial chromosome CC (YAC) vectors contain a reporter gene and transgenic mammals produced CC using them may be used to screen for an agent affecting nucleotide CC expression and gives easier monitoring of in vivo expression. The vector is used in the production of transgenic mammals for testing potential CC pharmaceutical or veterinary agents. pYAM4 is used to amplify YAC. The CC assay may be used to screen for agents useful in treatment of disturbance of circadian function, sleep disorders, eating disorders premenstrual CC dysfunction. The agents thus detected may be used for treatment of dysfunction. The agents thus detected may be used for treatment of CC disorders related to the expression pattern of a nucleotide such as those and more related to the expression pattern of a nucleotide such as those CC above. The vectors have more concentrated YAC DNA, which allows better and more related to the expression and the vectors allow for gene CC overexpression (3-5 fold) and easy site determination. The pyAM4 CC amplification vector does not contain the thymidine kinase gene, which could be caused male infertility in transgenic mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-1997;
20-MAR-1998;
05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New reporter gene labeled YAC vectors and transgenic mammals used screening potential active agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAC; yeast artificial chromosome; PCR primer; sexual dysfunction; reporter gene; transgenic mammal; therapy; circadian function; sleep disorder; eating disorder; premenstrual syndrome; birth defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a PCR primer used in the construction of a yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 56; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB2331752-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX57861 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MEDI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer used in construction of yeast artificial chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTCCCTCGCCTCCAGCCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schedl A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCCTCCTTTCCAGACACA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97GB-00025311.
97GB-00025313.
98GB-00006072.
98GB-00024275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98GB-00026126.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harmar AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.8%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 C; 1 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13.6;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Query Match

61

Score 13.6;

DB 2; Length 22;

Sequence

22

BP; 5 A; 11 C; 0 G; 6 T; 0 U; 0 Other;

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RESULT 14
AAC85242
The sequences given in AAC85227-50 are primers which were used to CC determine the size of the integrated YAC 35D8/D6 and YAC MSC7E526/V12 CC constructs in a transgenic founder animal. The constructs were prepared CC from novel yeast artificial chromosome (YAC) vectors each of which CC comprises a centromere, two telomeres, at least one origin of CC replication, an internal ribosomal entry site (IRES), and a selection CC gene that is specifically removable from the vector. The resulting YAC CC that can affect the expression pattern of a nucleotide sequence of CC interest (NOI) or the activity of its expression product. The identified agents are potentially useful as pharmaceutical and veterinary agents for CC treating disorders of circadian function; sleep or eating disorders; cCC premenstrual syndrome; autoimmune diseases; birth defects in women and/or CC excual dysfunction, and also as lead compounds for developing agents with CC compositions. The new vectors provide high YAC copy numbers and allow casy monitoring (in vivo) of the expression pattern of NOI; composition of NOI and a reporter gene; and determination of the stress where NOI is expressed. Incorporation of IRES allows expression of the than two nucleic acid sequences (e.g. NOI plus a reporter of more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-NOV-1997;
28-NOV-1997;
20-MAR-1998;
05-NOV-1998;
27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic organism for identifying potential therapeutic agents able to modulate gene expression, comprises a yeast artificial chromosome vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-034098/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB2350613-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reverse primer D 26376 for determining size of YAC insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC85242 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MEDI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               premenstrual syndrome; autoimmune disease; birth defect;
sexual dysfunction; serotonin transporter; VIP2 receptor; SEF
polymerase chain reaction; PCR; primer; amplify; YAC 35D8/D6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Internal ribosomal entry site; IRES; yeast artificial chromosome; YAC; vector; centromere; telomere; origin of replication; transgenic; vectorization function; sleep disorder; eating disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAC HSC7E526/V12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-2001
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                                                                        The invention discloses a microarray comprising a plurality of nucleic caid probes including one of 2,018,500 fully defined sequences, or its CC perfect match, perfect mismatch, antisense match or antisense mismatch. CC Also disclosed is a method of gene expression analysis. The array is used CC in monitoring gene expression levels by hybridisation to a DNA library. CC in analysis of genetic variation or in hybridisation to a DNA library. CC in analysis of genetic variation or in hybridisation to a DNA library. CC in analysis of genetic variation or in hybridisation to a DNA library. CC of at least one target sequence. The method of analysis comprises CC of at least one target sequence. The method of analysis comprises CC incleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid CC gene expression levels, identifying biallelic markers or polymorphisms, CC or family members of a gene and a cross-species comparises monitoring CC gene expression to identify or detect the sequence. The array of nucleic acid could be supported in in situ hybridisation, in Southern, Northern or dotonot hybridisation to identify or detect the sequence or specific CC mutations of any gene, in mapping the 5' termini of mRNA molecules by CC primer extensions or in screening cDNA or genomic libraries or subclones CC isolated and previously sequenced. The sequence of the collated and probes incorporated in the microarray. Note: The sequence CC data for this patent can also be obtained in electronic format directly cross the collated and sequence of sequence of the collated sequence of the collated sequence of the collated sequence of the collated sequence of the sequence of the collated sequence of the collated sequence of the sequence of the collated sequence of the sequence of the collated sequence
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    41078325 seqs, 23393541228 residues
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Gapop 10.0 , Gapext 1.0
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9b est2:
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CC9730897
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AZ332711 IN0061814
AZ788256 2M0035A17
CZ477475 d10866-3p
AZ980990 2M025871
AZ655652 IM0530D13
AA864650 0h37b09.s
AI158446 ud28b12.r
AW247040 2822414.5
AZ8653707 2M0171N1.9
AI279523 q151d12.x
AZ498825 IM0336J14
BG926661 HMC23-1-E
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AZ4404465 IM0172D09
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AZ4439789 IM0230004
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10.6	10.6	10.6	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.8	11	11	11	11	11	11	11	11	11	11
48.2	48.2	48.2	49.1	49.1	49.1	49.1	49.1	49.1	49.1	49.1	49.1	49.1	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
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# ALIGNMENTS

	FEATURES source			TITLE JOURNAL COMMENT	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 CG730897/c LOCUS DEFINITION ACCESSION
/organism="Lea mays" /ord type="genomic DNA" /cultivar="mixed background w23/A188/B73/K55" /db xref="taxon:4577" /tissue type="leaf" /dev stage="adult" /lab_host="DH10B" /clone lib="1119 - RescueMu Grid AA" /clone lib="1119 - RescueMu Grid AA" /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for	Location/Qualifiers	POSSIDLE 1194TION SITE OF ENGS CUT BY 2 GIFFERENT ENGONUCLEASES. REVERSE COMPLEMENTED POST-LIGATION SEQUENCE FROM SOURCE SEQUENCE. Plate: 1119130 row: F column: 05 Class: transposon-tagged.	Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel. 650 733 2227	Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V	Sperimarophyra; magnorrophyra; miropsida; roares; roaceae; raccan clade; Panicoideae; Andropogoneae; Zea.  1 (bases 1 to 25) Walbot,V.	CG730897.1 GI:37773389 GSS. Zea mays	CG730897 25 bp DNA linear GSS 20-OCT-2003 1119130F05.2EL x1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence. CG730897

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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid end-
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CL676355
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GSS.
AZ762096 24 bp DNA linear GSS 16-FEB-200 IM0556018R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0556J18 R, genomic survey sequence.

AZ762096 AZ762096.1 GI:12871740
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Contact: Sommer RJ
Evolutionary Biology
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Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CL676355 29 bp DNA linear GSS 09-JUL-2004 PRI0118b_E09_2 - PRI0118b_BR (29) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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                                                                                                                                                                                                                                                                                                                                                                                /organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                            /note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                              /clone_lib="Mixed stage var. California"
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Pred. No. 2e+05;
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Pred. No. 1.1e+06;
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AI416870
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AI416870 25 bp mRNA linear EST 23-JUL-2 sal9b03.xl Gm-c1005 Glycine max cDNA clone GENOME SYSTEMS CLONE Gm-c1005-102 3' similar to TR:Q39599 Q39599 EXTENSIN. ;, mRNA
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High quality sequence stop: 24.
Location/Qualifiers
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Mus musculus (house mouse)
Mus musculus
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Insert Length: 10000 Std Error: (
Plate: 0556 row: J column: 18
Seq primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /Clone_lib="Mouse 10kb plasmid UUGCM library" /note="Vector: pWD42Inv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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75.0%;
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AI416870.1
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. GENOME SYSTEMS CLONE ID: Gm-c1005-102 Trace considered overall poor quality Possible reversed clone: similarity on wrong strand This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Seq primer: T7 ET from Amersham High quality sequence stop: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Guovanne Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                       D21049 25 bp mRNA linear EST 30-JUL-1996
HUMGS02034 Human promyelocyte Homo sapiens cDNA clone mp0338 3',
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Fax: 314 286 1810
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Hominidae; Homo
                                                                                               domo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /notes Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; This library was constructed by Dr. Randy C. Shoemaker and Dr. John Erpelding, USDA-ARS Agronomy Department, G401 Agronomy Hall, Iowa State University, Ames, IA 50011-1010 Phone: 515-294-6233 FAX: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     email: rcsshoe@iastate.edu<sup>=</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="XL10-Gold"
/clone_lib="Gm-c1005"
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clone="GENOME SYSTEMS CLONE ID: Gm-c1005-102"
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Pred. No. 1.7e+06;
0; Mismatches 5;
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DEFINITION
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Unpublished (2000)
Contact: Robert B. University of Utah (University of Utah
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Dunn,D., Aoyagi.A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ332711 29 bp DNA lineau 100061N14F Mouse 10kb plasmid UUGC1M library Mus clone UUGC1M0061N14 F, genomic survey sequence.
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Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed
                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0061 row: N column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
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Yoshinari,H., Arimoto,J. and Matsubara,K.
Institute for Molecular and Cellular Biology
Osaka University
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Unpublished (1993)
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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308,
USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Human promyelocyte"
/note="Female, adult, cell_line = HL60, cell_type =
promyelocyte. "
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0061N14"
                                                       organism="Mus musculus'
/mol_type="genomic DNA"
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/db_xref="taxon:9606"
/clone="mp0338"
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75.0%;
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Pred. No. 1.7e+06;
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Insert Length: 10000 Std Error:
Plate: 0035 row: A column: 17
Seg primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 29)
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29 bp DNA linear GSS 16-FEB-200 2M0035A17F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0035A17 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
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                                                                                                                                                                         quality sequence stop: 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative aggrose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                    plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                           /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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lab_host="E. Coli strain XL10-Gold, T1-resistant,
xref="taxon:10090"
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RESULT 7

ORIGIN

Matches

JOURNAL COMMENT

TITLE

FEATURES

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SOURCE

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CZ477475
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

(bases 1 to 29)

Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A., Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L., Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L., Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L., Singh,C.M., Buchholz,R., Homes, J., Fisher,W.W., Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K., Greer,R., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C., Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F., Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F., Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.L. and Margolis,J. A complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                          Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CZ477475 29 bp DNA linear GSS 29-APR-20 d10866-3prime Exelixis P element XP insertions Drosophila melanogaster genomic Sequence recovered from 3' end of P element,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
The P element insertion position is 1 in the 29 bases. This insertion position refers to the first base of the 8 base target
                                                                                     Sequence recovery method was inverse Sequence orientation is forward strar
                                                                                                                                                                                                                                                                                                                                                                                              using P and piggyBac Nat. Genet. 36 (3), 2
                                                                                                                                                    Email: RHoskins@lbl.gov
                                                                                                                                                                                                                                                                                                                                        Contact: Roger A Hoskins
                                                                                                                                                                                                                                                                                                                                                                     14981521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CZ477475.1 GI:62972885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (gi 4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/Clome_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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75.0%;
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Pred. No. 1.7e+06;
                                                                                           strand relative to 5'
                                                                                                                        PCR.
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                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 025B row: F column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
Unpublished (2000)
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2M0258F17F Mouse 10kb plasmid UUGC2M library Mus musculus
clone UUGC2M0258F17 F, genomic survey sequence.
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                                                                                                                                                                 High quality sequence stop: 22.
Location/Qualifiers
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/db xxef="taxon:7227"
/clone lib="Exelixis P element XP insertions"
/note="Vector: P element XP (GenBank accession number AY5.5149), An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinscy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."
                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                             organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/mol_type="genomic_DNA"
/strain="isogenic_w-_strain"
lab_host="E. coli strain XL10-Gold, T1-resistant,
                                        clone="UUGC2M0258F17"
                                                              db_xref="taxon:10090"
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75.0%;
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Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                 Std Error:
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                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0530 row: D column: 13
Seq primer: CAFACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert B. University of Utah University of Utah
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                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus C57BL/6J (female) was obtained from the Jackson
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 11.6; DB 9;
Pred. No. 2.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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/db\_xref="taxon:10090"

clone="UUGC1M0530D13"

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Query Match
                                                                                                                                                                                                          source
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AA864650

CAP Kid6 Homo sapiens CDNA Clone IMAGE:1459961 3'

Similar to SW:ATPQ_BOVIN P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 952 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA864650.1 GI:2958963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae, Homo.
1 (bases 1 to 28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
                                                                                                                                                                                                                                                                                               ert Length: 952 Std Error: 0.00
primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                   quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt end-sin high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv, Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
                                                        'sex="mixed"
                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
tissue_type="kidney tumor"
/lab_host="SOLR (kanamycin resistant)"
                                                                                    clone="IMAGE:1459961"
                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.8%;
71.4%;
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Pred. No. 3e
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ACCESSION VERSION

KEYWORDS

DEFINITION

POCUS AA864650/c

RESULT 11

SOURCE ORGANISM

REFERENCE

COMMENT

JOURNAL TITLE AUTHORS

FEATURES

밁 ঠ ORIGIN

Matches

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REFERENCE
AUTHORS
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VERSION
KEYWORDS
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AI158446
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 28)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.,
Waterston, R.,
The Macket Company of the Market C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ud28b12.r1 Soares mammary_gland_NbMMG Mus IMAGE:1447199 5' Similar to SW:CAV2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trace considered overall poor quality Possible reversed clone: similarity on wrong Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
IMAGE Consortium (info@image.llnl.gov) for further
MGI:920515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI158446.1 GI:3686915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Kid6"
/note="Organ: kidney; Vector: Bluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5'
GAATTCGGCACGAG 3' 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."
                                                                                                         T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector.
                                                                                                                                                                                                                                                                                                                       /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:10090"
clone="IMAGE:1447199"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mol_type="mRNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ion/Qualifiers
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AW247040/c
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Matches 13; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL Unpublished (1999)
Other_EST8: 2822414.3prime
Other_EST8: 2822414.3prime
Contact: Robert Stransberg, Ph.D.
Email: Ggapbs r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center
Trimming: cross match from University of Washingtion Genome Center
PHRAP suite. Poly-T Identification: pathwatch.pl from Berkeley
Drosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 15
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 16 contiguous distinct
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High quality sequence stop: 15.
Location/Qualifiers
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1 (bases 1 to 16)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene
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2822414.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822414 5',
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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       Conservative
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                                                                                                                    /lab host="DH108 (phage-resistant)"
/clone libs "NIH_MGC 7"
/clone libs "NIH_MGC 7"
/clone Torgan: lung; Vector: pOTB7; Site 1: XhoI; Site 2: /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:2822414"
/tissue_type="small cell carcinoma"
/cell_lIne="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                             50.9%;
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92.3%;
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0; Mismatches 3
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                                               Length 16;
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     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ863707
2M0171N19R Mouse 10kb plasmid clone UUGC2M0171N19 R, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0171 row: N column: 19
Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: plasmid ends
High quality sequence stop: 22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
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801 585 7177
                                                                                         Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /Clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: pW1042nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC2M0171N19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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50.9%;
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Score 11.2; DB 9;
Pred. No. 3.6e+06;
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AUTHORS
TITLE
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AI279523
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Search completed: March 25, Job time: 3043.5 secs
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ORGANISM
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Best Local Similarity
Matches 13; Conserv
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 588 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers
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28 bp mRNA linear EST 29-JAN-1999 q151d12.x1 Soares NhHMPu S1 Homo sapiens cDNA clone IMAGE:1875863 3' similar to SW:EXTN TOBAC P13983 EXTENSIN PRECURSOR ;contains MER22.b1 MSR1 repetitive element ;, mRNA sequence.
A1279523
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                            /clome lib="Soares NhHMPu S1"
/note="Organ: mixed (see Delow); Vector: pT7T3D-Pac
/note="Organ: mixed (see Delow); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified CDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1875863"
                                                                                                                                                                                    50.9%; Score 11.2; DB 1; Length 28; 81.2%; Pred. No. 3.6e+06; ive 0; Mismatches 3; Indels
                         2006, 15:28:19
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re greater than or equal to the score of the result being printed,
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6h_COMB.seq:*
/cgn2_6/ptodata/1/ina/6h_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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US-08-462-040-12
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US-09-119-507B-10
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Sequence 19, Appl
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Sequence 12, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 58648, A
Sequence 58650, A
Sequence 10, Appl
Sequence 38, Appl
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Sequence 61491, A	Sequence 56734, A	Sequence 43716, A	e 4371	Sequence 19, Appl		۲	Sequence 61, Appl		φ,	Sequence 17, Appl	Appl	Sequence 6, Appli	Sequence 4, Appli	•	Sequence 44454, A	Sequence 2327, Ap	•	•	Sequence 8, Appli	-

## ALIGNMENTS

US-08-460-890A-19/c ; Sequence 19, Application US/08460890A ; Patent No. 5994109 ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARB: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U\$/08/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
APTLICATION NUMBER: PCT/US93/02725
APPLICATION NUMBER: PCT/US93/02725 TELEFAX: (213) 955-044
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440 STREET: 633 West Fifth St STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A GENERAL INFORMATION: SEQUENCE CHARACTERISTICS: APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRITITE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 212/066 ACID TRANSPORTER SYSTEMS AND

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Best Local Similarity 80.0
Matches 16; Conservative
Query Match
Best Local Similarity
Matches 16; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
CTPANITATION of CITY
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OPERATING SYSTEM: FIRM P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,890A
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
                                                                                                                  TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600 TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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COUNTRY:
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                          NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/066
                                                                                                                                                           STRANDEDNESS: single
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Score 13.6; DB 2;
Pred. No. 1.2e+04;
0; Mismatches 4
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                                             DB 2; Length 27;
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Gaps
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RESULT 4
US-08-167-641C-22/c
US-08-167-641C-22/c
; Sequence 22, Application US/08167641C
; Patent No. 6033884
; Patent No. 6033884
; GENERAL INFORMATION:
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; Sequence 19, Application US/08167641C
; Patent No. 6033884
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                                                                                                                                                                                                           Query Match 61.8%;
Best Local Similarity 80.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASUSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,389
PILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
APPLICATION NUMBER: 907/US93/02725
APPLICATION NUMBER: 20, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 305/012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                        TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NUCLEIC ACID TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: SIL
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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Gottchalk, Stephen
VENTION: NUCLEIC AC
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                                                                                                                                                                                                                                                                                                                                                                                                                19:
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                                                                                                                                                                                                             Score 13.6; DB 3;
Pred. No. 1.2e+04;
0; Mismatches 4;
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                                                                                                                                                                                                                                               Length 27;
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APPLICANT: Woo, Savio L.C.

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TELEFAX: (41.)
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
TYPE: nucleic single
                                                                                                                                                                                                                                                                                                            US-08-460-971A-19/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-167-641C-22
                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                            GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: MUCLEIC ACID TRANSPORTER SYSTEMS
TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C FILING DATE: December 14, 1993
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: BH Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
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APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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Local Similarity 80.0%;
eB 16; Conservative
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STREET: Suite 4700
CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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o. 6150168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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OPERATING SYSTEM: IBM P.C. DOS:
SOFTWARE: FASTENCY IBM P.C. DOS:
SOFTWARE: FASTENCY IBM P.C. MINDOWS 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,9:
PILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/027
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: March 19, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTMARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,971A
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                              APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (213) 489-16
TELEFAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                        COUNTRY: U.S.A.
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80.0%; Pred. No. 1.2e+04;
tive 0; Mismatches 4;
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-460-971A-22
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
APPLICATION NUMBER: PCT/US93/02725
APPLICATION NUMBER: DET/US93/02725
APPLICATION NUMBER: 32,327
RETERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/063
TELEPHONE: (213) 489-1600
TELEPAX: 67,1510
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
                                                                                                                                                                                                                                                                                                                                            CLL.
STATE: U.S...
COUNTRY: U.S...
TP: 90071-2066
PEADABLE F
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: SULLE CITY: LOS Angeles CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WOO, Savio L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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US-08-462-040-22/c
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TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
; SEQUENCE CHARACTERISTICS:
; FRIGHT: 27 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                         COUNTRY: U.S.A.

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: BM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSEQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/462,040

FILING DATE: June 5, 1995

CLASSIFICATION NUMBER: 08/167,641

PRIOR APPLICATION NUMBER: 08/167,641

PRIOR APPLICATION NUMBER: 07/853,389

PRICHOR DATE: MARCH 20, 1992

APPLICATION NUMBER: DT/US93/02725

APPLICATION NUMBER: DT/US93/02725

FILING DATE: MARCH 19, 1993

ATTORNEY/AGENT INFORMATION:

MACHINE MARCH 19, 1993

ATTORNEY/AGENT INFORMATION:
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APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: METHODS OF USE
TITLE OF INVENTION: METHODS OF USE
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                       REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 633 West FI
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                    TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (213) 489-101
TELEFAX: (213) 955-0440
                                                                                                                                                NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 61.8%;
Local Similarity 80.0%;
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5. 6177554
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                                             67-3510
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Pred. No. 1.:
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APPLICANT: AFFMENTIX, Inc.
APPLICANT: AFFMENTIX, Inc.
FILE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 58649
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: nucleic acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-462-040-22
                                                                    ; ORGANISM: mus musculus US-09-396-196G-58649
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US-09-396-196G-58648, Application US/09396196G
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CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
SEQ ID NO 58648
LENGTH: 25
   Query Match 60.9%;
Best Local Similarity 93.3%;
Matches 14; Conservative
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Matches
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                                                                                                                                                                                                                                                                                        APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Michael Mittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
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APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 61.8%;
Local Similarity 80.0%;
hes 16; Conservative
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Local Similarity 93.3%;
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 Score 13.4; DB 3;
Pred. No. 1.4e+04;
0; Mismatches 1;
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Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                 Length 25;
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   Indels
 <u>,</u>
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Gaps
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APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
ITITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
FRIOR APPLICATION NUMBER: 60/100,678
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 58650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-766-982-10
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; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-58650
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                                                             APPLICATION NUMBER: US/08/
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Appl
Patent No. 59488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 58650, Appropriate No. 682172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wahl, Robert C.
TITLE OF INVENTION: Analogs of Macrophage Stimulating
TITLE OF INVENTION: Protein
TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 60.9%;
Local Similarity 93.3%;
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                                                                                                                                                                                                                                                                                                                                 91320-1789
                                               nucleic acid
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                                                                                                                                                                                                                                                                                                                                                   USA
                  linear
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Pred. No. 1.4e+04;
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RESULT 13
US-09-296-219-10
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                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-296-219-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: P.
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 76.2
                                                                                                                                                                Sequence 16, Application US/08529190B Patent No. 5833991
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/09296219 Patent No. 6248560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Re-lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1890 CITY: Thousand Oaks
STATE: California
                                                                        NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd
                                                                                                                      APPLICANT: MASUCCI, MARIA G.
TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES
TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wahl, Robert C.
TITLE OF INVENTION: Analogs of Macrophage Stimulating
TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                            CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
COUNTRY: U
                                                            STREET:
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1840 Dehavilland Drive
                                                            One Financial Center
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76.2%;
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; Pred. No. 2.1e
0; Mismatches
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Pred. No. 2.1e+04;
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US-09-119-507B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-529-190B-16
                                                                                                                                                                 SEQ ID NO 10
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia J.
TITLE OF INVENTION: No. 6548642el
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/09119507B Patent No. 6548642
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OPERATING SYSTEM: DOS
SOFTWARE: WORDERECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,190B
FILING DATE: 15-SEP-1995
CLASSIFICATION DATA: SE9501324-9
FILING DATE: 10-APR-1995
APPLICATION NUMBER: US08/522,595
FILING DATE: 01-SEP-1995
APPLICATION NUMBER: US08/522,595
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen A
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3255/53015
                                                                                                                                                                                                                                                  FILE REFERENCE: OHU-03417
CURRENT APPLICATION NUMBER: US/09/119,507B
CURRENT FILING DATE: 1998-07-20
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: si
TOPOLOGY: linear
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                               1 CTCCCTCGCCTCCAGCCACAT 21
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CACCTTCACCTCCACCCCCAT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617-345-9100
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                                                                               59.1%;
76.2%;
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Pred. No. 2.1e+04;
                                                                 Score 13; DB 3; Le
Pred. No. 2.1e+04;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                Length 30;
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                                                                                                                                                   Synthetic
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Search completed: March 25, Job time: 129.5 secs

2006, 13:03:00

#### November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases: older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions ... rnpbm (Published\_Applications\_NA\_Main) and .rnpbn (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_Main) and .rapbn (Published\_Applications\_AA\_New).



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Result
No.
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Maximum |
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                nucleic search, using sw model
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/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
          Applications_NA_Main:*
                           US-11-036-317-589884
US-11-036-317-179644
US-11-036-317-250919
US-11-036-317-253919
US-11-036-317-268615
US-11-036-317-362146
US-11-036-317-391184
US-11-036-317-391184
US-11-036-317-278200
US-11-036-317-2800075
US-11-036-317-2800075
US-11-036-317-36952
US-11-036-317-36952
US-11-036-317-469308
US-11-036-317-469308
US-11-036-317-574241
US-11-036-317-574236866
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US-10-798-652-6
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                                                                 Sequence 7, Appli
Sequence 6, Appli
Sequence 19844,
Sequence 250940,
Sequence 253919,
Sequence 253919,
Sequence 361146,
Sequence 391146,
Sequence 20, Appl
Sequence 278200,
Sequence 278200,
Sequence 286177,
Sequence 386177,
Sequence 360952,
Sequence 469308,
Sequence 674241,
Sequence 20618, A
Sequence 20618, A
Sequence 20618, A
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                           Sequence
Sequence
          693282,
; Sequence 6, Application US/10798652; Publication No. US20040219582A1
; GENERAL INFORMATION; GENERAL INFORMATION; APPLICANT; Yongjun Guo
; TITLE OF INVENTION; FGP-3 GENE AND METHODS OF USE THEREOF; FILE REFERENCE; 3382-P03136US01
; CURRENT APPLICATION NUMBER; US/10/798,652
; CURRENT FILING DATE; 2004-03-11
; PRIOR APPLICATION NUMBER: 60/455,698
; PRIOR APPLICATION NUMBER: 60/455,698
; PRIOR FILING DATE; 2003-03-17
; NUMBER OF SEQ ID NOS; 7
                                                                                                                                                                                                                                                                                             RESULT 2
US-10-798-652-6
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US-10-215-112-12019	US-11-036-317-579816	US-11-036-317-579814	US-11-036-317-516615	US-10-956-157-163759	US-10-719-900-16414	US-09-940-185-956	US-11-036-317-923714	US-11-036-317-516736	US-10-956-157-250478	US-10-956-157-174568	US-10-485-048-86	US-10-681-773-72893	US-10-681-773-22338	US-11-036-317-846119	US-11-036-317-589885	US-11-036-317-343201	US-11-036-317-70925	US-10-956-157-257895	US-10-956-157-257894	US-10-956-157-252303	US-10-956-157-212800
Sequence 12019, A	Sequence 579816,	Sequence 579814,	Sequence 516615,	Sequence 163759,	Sequence 16414, A	Sequence 956, App	Sequence 923714,	Sequence 516736,	Sequence 250478,		Sequence 86, Appl	Sequence 72893, A	Sequence 22338, A	Sequence 846119,	Sequence 589885,	Sequence 343201,	æ	Sequence 257895,	Sequence 257894,	Sequence 252303,	Sequence 212800,

ALIGNMENTS

#### Sequence 7, Application US/10798652 Publication No. US20040219582A1 GENERAL INFORMATION: APPLICANT: Yongjun Guo TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISM IN THE TITLE OF INVENTION: FGF-3 GENE AND METHODS OF USE THEREOF FILE REFERENCE: 3382-PO3136US01 CURRENT APPLICATION NUMBER: US/10/798,652 CURRENT FILING DATE: 2004-03-11 PRIOR APPLICATION NUMBER: 60/455,698 PRIOR FILING DATE: 2003-03-17 NUMBER OF SEQ ID NOS: 7 SOFTWARE: FastSEQ for Windows Version 3.0 LEGUID OT Query Match Best Local Similarity Matches 22; Conserva LENGTH: 22 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: probe μ 1 CTCCCTCGCCTCCAGCCACATG 22 CTCCCTCGCCTCCAGCCACATG Conservative 100.0%; Score 22; DB 100.0%; Pred. No. 12; 0; Mismatches æ ,-Length 22 Indels 0

Gaps

0

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Sequence 179644, Application US/11036317

Publication No. US20050214823A1

GENERAL IMFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John

ITILE OF INVENTION: Method of Analysis of Alternative Splicing
FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT EILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 179644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 589884, Application US/11036317

PUBLICATION NO. US20050214823A1

GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
ITILE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1

CURRENT APPLICATION NUMBER: US/11/036,317

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 589884
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US-11-036-317-179644/c
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                                                                    ; ORGANISM: Mus musculus 
US-11-036-317-179644
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Query Match
Best Local S
Matches 18
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LENGTH: 22
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Best Local Similarity
Matches 21; Conserv
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Best Local (
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                                                                                                       TYPE: DNA
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                                                                                                                       LENGTH:
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Local Similarity 89.5%;
Local Similarity 81.
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95.5%;
                  70.9%;
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Pred. No. 5
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Pred. No. 4.
Score 15.6; DB 10
Pred. No. 5.9e+03;
0; Mismatches 4
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                                  DB 10;
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RESULT 6
US-11-036-317-253919/c
; Sequence 253919, Application US/11036317
; Publication No. US20050214823A1
; Publication No. US20050214823A1
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                                                                                                                                      RESULT 7
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CURRENT FILING NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 250940
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1 SEQ ID NO 253919
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APPLICANT: Williams, Alan
APPLICANT: Blume, John
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                                                                                Sequence 268615, Application US/11036317 Publication No. US20050214823A1
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Best Local Similarity
                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                             Best Local Similarity
APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
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APPLICANT: Blume, John
TITLE OF REPERIOR 1001. Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
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ORGANISM: Mus musculus
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0; Mismatches
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Pred. No. 5.9e+03;
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APPLICANT: Williams, Alan
APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splic
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 362146
LENGTH: 25
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; ORGANISM: Mus musculus
US-11-036-317-362146
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US-11-036-317-391184
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US-11-036-317-362146
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US-11-036-317-268615
                                                                     GENERAL INFORMATION:

APPLICANT: Williams, Alan

APPLICANT: Williams, Alan

APPLICANT: Blume, John

TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse

FILE REFERENCE: 3654.1

CURRENT FILING DATE: 2005-01-13

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR APPLICATION NUMBER: US 60/536,639

PRIOR FILING DATE: 2004-01-13

NUMBER OF SEQ ID NOS: 991174

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 391184
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CURRENT PILLING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR RILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 268615
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                Sequence 391184, Application US/11036317 Publication No. US20050214823A1
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Best Local Similarity
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Best Local Similarity 81.8%;
Matches 18; Conservative
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TYPE: DNA
ORGANISM: Mus musculus
·11-036-317-391184
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                                                          ENGTH: 25
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81.8%; Pred. No. 5.9e+03
Live 0; Mismatches
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Pred. No. 5.9e+03;
0; Mismatches 4
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RESULT 12
US-11-036-317-278200/c
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; Sequence 19930, Application US/11060756
; Publication No. US20050221354A1
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Best Local S
Matches 16
                                                                                                                                                                                                                                  SEQ ID NO 20
LENGTH: 20
TYPE: DNA
ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/10994138
Publication No. US20050186666A1
GENERAL INFORMATION:
APPLICANT: Dow Global Technologies, Inc.
TITLE OF INVENTION: Improved Protein Expression Systems
FILE REFERENCE: 00588.105020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.2
SEQ ID NO 199930
LENGTH: 25
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Best Local Similarity
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AMADIO83 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
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Best Local Similarity
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CURRENT FILING DATE: 2004-11-19
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SOFTWARE: PatentIn version 3.2
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                                                                                CTCGCCTCCAGCCACAT 21
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                                                              CTCGCCTCCTGCCACAT 17
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Pred. No. 7.4e
0; Mismatches
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Sequence 278200, Application US/11036317 Publication No. US20050214823A1 GENERAL INFORMATION:

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RESULT 14
US-11-036-317-280075
; Sequence 280075, Application US/11036317
; Sequence 280075, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 280075
; TUDE: NOWARE: 25075
; TUDE: NOWARE: 25075
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US-11-036-317-386177/c
; Sequence 386177, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
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; ORGANISM: Mus musculus
US-11-036-317-386177
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APPLICANT: Blume, John
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
TILE REFERENCE: 3654.1
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 386177
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 278200
LENGTH: 25
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Best Local Similarity 85.0%;
Matches 17; Conservative
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TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR PILING DATE: 2004-01-13
PRIOR FILING DATE: 2004-01-13
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TYPE: DNA
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17; Conserv
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Pred. No. 8.6e+03
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Pred. No. 8.6e+03;
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ORGANISM: Mus musculus

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Search completed: March 25, Job time: 661.5 secs
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US-11-036-317-360952
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                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse FILE REFERENCE: 3654.1
CURRENT APPLICATION NUMBER: US/11/036,317
CURRENT FILING DATE: 2005-01-13
PRIOR APPLICATION NUMBER: US 60/536,639
PRIOR FILING DATE: 2004-01-13
NUMBER OF SEQ ID NOS: 991174
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 360952
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
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Best Local Similarity 81.0%;
Matches 17; Conservative
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                                                                                                                                                                                                                                           TYPE: DNA
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Local Similarity 81.0%;
ses 17; Conservative
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                                                                     TCCCTCCCATGCAGCCACCTG
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Pred. No. 1.5e+04;
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /SIDSS/ptodata/1/pubpna/US06_NI

2: /SIDSS/ptodata/1/pubpna/US07_NI

3: /SIDSS/ptodata/1/pubpna/US07_NI

4: /SIDSS/ptodata/1/pubpna/US07_NI

5: /SIDSS/ptodata/1/pubpna/US09_NI

6: /SIDSS/ptodata/1/pubpna/US10_NI

8: /SIDSS/ptodata/1/pubpna/US10_NI

9: /SIDSS/ptodata/1/pubpna/US10_NI

10: /SIDSS/ptodata/1/pubpna/US10_NI

9: /SIDSS/ptodata/1/pubpna/US11_N

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   Listing
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| SIDSS/ptodata/1/pubpna/US07 NEW PUB.seq:*
| SIDSS/ptodata/1/pubpna/US07 NEW PUB.seq:*
| SIDSS/ptodata/1/pubpna/US09 NEW PUB.seq:*
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| SIDSS/ptodata/1/pubpna/US10 NEW PUB.seq:*
| SIDSS/ptodata/1/pubpna/US10 NEW PUB.seq:*
| SIDSS/ptodata/1/pubpna/US10 NEW PUB.seq:*
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   GenCore version (c) 1993 - 2006
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US-10-310-914A-743419

US-10-310-914A-743458

US-10-310-914A-299068

US-10-310-914A-631446

US-10-310-914A-631446

US-10-310-914A-533742

US-10-310-914A-549830

US-10-310-914A-549830

US-10-310-914A-549844

US-10-310-914A-213337

US-10-310-914A-213337

US-10-310-914A-213338

US-10-310-914A-21338

US-10-310-914A-668834

US-10-310-914A-668839

US-10-310-914A-213339

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US-10-310-914A-668839

US-10-310-914A-213339

US-10-310-914A-213339
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Sequence 148615,
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Sequence 177473,
Sequence 631446,
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668834,
969892,
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317759,
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Publication No. US20060003322A1

GENERAL INFORMATION:

APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kyuzat

TITLE OF INVENTION: Bioinformatically detectable group of:

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT SEQ ID NOS: 1388402

SOFTWARE: PatentIn version 3.3

SEQ ID NO 613434

LENGTH: 20

ORGANISM: Human

ORGANISM: Human
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64.5	64.5			64.5				64.5	65.5	65.5	65.5	65.5	65.5	65.5	65.5	66.4	66.4	66.4	66.4	67.3	67.3	67.3	67.3	67.3	67.3	67.3
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US-10-310-914A-1352505	US-10-310-914A-724597	US-10-310-914A-1352507	US-10-310-914A-1223911	US-10-310-914A-1002041	US-10-310-914A-519040	US-10-310-914A-448406	US-10-310-914A-654165	US-10-310-914A-372336	US-10-933-982-36071	US-10-310-914A-782816	US-10-310-914A-782776	US-10-310-914A-532862	US-10-310-914A-102291	US-10-310-914A-102269	US-10-310-914A-532861	US-10-857-780-2372	US-10-310-914A-91863	US-10-310-914A-91862	US-10-310-914A-237510	US-11-121-849-439265	US-10-310-914A-1138594	US-10-310-914A-1108644	US-11-093-746A-14	US-10-310-914A-1138593	US-10-310-914A-701328	US-10-310-914A-377554
Sequence 1352505	Sequence 724597,	Sequence 1352507	Sequence 1223911	Sequence 1002041	Sequence 519040		Sequence 654165	Sequence 37233	Sequence 36071	78281	æ			Sequence 102269		Sequence 2372,	Sequence 91863	Sequence 91862	Sequence 237510	Sequence 439265	Sequence 1138594	_	O		Sequence 701328	Sequence 37755
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### ALIGNMENTS

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US-10-310-914A-148615

Sequence 148615, Application US/10310914A

Publication No. US20060003322A1

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable
TITLE OF INVENTION: uses thereof
TILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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2 CCCUGACCUCCAGCCACAU 20
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                                                                                   of novel regulatory genes
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and

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APPLICANT: Shiler, Kvuzat
ITITLE OF INVENTION: Bioinformatically detectable granted of INVENTION: Bioinformatically detectable granted of INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 743458
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; ORGANISM: Human
US-10-310-914A-148615
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                                                                 Query Match
Best Local S
Matches 16
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APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: Uses thereof
TILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 743419
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Best Local Similarity
Matches 15; Conserv
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 148615
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Best Local (
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TYPE: RNA
ORGANISM: Human
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ORGANISM: Human
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 CTCCCTCGCCCCCAGCC 2
                               CTCCCTCGCCTCCAGCC 17
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Pred. No. 1.
                                                                                 Score 15.4; DB 8; Pred. No. 2.8e+03;
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Pred. No. 1.
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; Sequence 290068, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of
; TITLE OF INVENTION: uses thereof
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                              US-10-310-914A-631446
Sequence 631446, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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Sequence 177473, Application US/10310914A

Publication No. US20060003322A1

; GENERAL INFORMATION:
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US-10-310-914A-290068
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILIG DATE: 2002-12-06
UNMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 177473
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Matches
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SEQ ID NO 290068
LENGTH: 20
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Best Local Similarity
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APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detec
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
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nilarity 80.0%;
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Pred. No. 3.4e
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                                                              Query Match
Best Local S
Matches 15
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 233742
LENGTH: 24
                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 549830
LENGTH: 24
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 549830, Application US/10310914A
Publication No. US20060003322A1
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Best Local (
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                                                                                                                                                                                                                                                         APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 066087.0200.CPUS01
FILE REFERENCE: 066087.0200.CPUS01
                                                                                                                                             ORGANISM: Human
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ORGANISM: Human
                                                                                                                                                           TYPE: RNA
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                                                                               Similarity
                              CTCCCTCGCCTCCAGCCACA 20
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; Pred. No. 3.4e-
2; Mismatches
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                                                                             Score 15.2;
Pred. No. 3.
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                                                            Mismatches
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APPLICANT: Bentwich, Isaac

APPLICANT: Shiler, Kvuzzt

APPLICANT: Shiler, Kvuzzt

TITLE OF INVENTION: Bioinformatically detectable gro

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 06087.0200.CPUS01

CURRENT APPLICATION NUMBER: US/10/310,914A

CURRENT FILING DATE: 2002-12-06

NUMBER OF SEQ ID NOS: 1388402

NUMBER OF SEQ ID NOS: 1388402
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US-10-310-914A-213337/c
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; Sequence 165922, Application US/10310914A
; Publication No. US20060003322A1
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                                                                                                                                                                                                        Sequence 213337, Application US/10310914A Publication No. US20060003322A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.3 SEQ ID NO 165922
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
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ORGANISM: Human
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TYPE: RNA
ORGANISM: Human
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75.0%;
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RESULT 13
US-10-310-914A-120157/c
US-10-310-914A-120157, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
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                                                                                                                                                          Sequence 213338, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 213338
LENGTH: 19
TYPE: RNA
ORGANISM: Human
ORGANISM: Human
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APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 120157
LENGTH: 19
TYPE: RNA
ORGANISM: Human
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Best Local S
Matches 16
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Matches 16; Conservative
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LENGTH: 18
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Best Local Similarity
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ORGANISM: Human
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                                                                       67.3%; Score 14.8; DB 8;
88.9%; Pred. No. 5.1e+03;
tive 0; Mismatches 2;
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88.9%; Pred. No. 5.1e+03;
tive 0; Mismatches 2; Indels
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US-10-310-914A-668834/c
US-10-10-914A-668834, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
                                                                                                                                                                                            APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 668834
LENGTH: 19
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                                                                                                                                                                 TYPE: RNA
ORGANISM: Human
18
                                                                   16; Conservative
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Pred. No. 5.1e+03;
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1: /SIDS5/ptodata/1/pubpna/US06_NEW_PUB.seq:*

2: /SIDS5/ptodata/1/pubpna/US07_NEW_PUB.seq:*

3: /SIDS5/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /SIDS5/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq:*

6: /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq:*

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6 US-09-925-065A-734471
14 US-11-121-086-20
8 US-10-750-185-32987
8 US-10-750-623-32987
6 US-09-925-065A-57042
9 US-10-301-480-158280
10 US-10-301-480-771689
8 US-10-995-561-69610
9 US-10-995-561-69610
9 US-10-995-561-13412
10 US-10-995-561-13464
11 US-11-121-086-91
9 US-10-995-561-3364
12-10-301-480-93596
10 US-10-905-561-3364
10 US-10-301-480-93596
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Biocceleration Ltd.
Sequence 61, Appl
Sequence 734471,
Sequence 32,987, A
Sequence 32987, A
Sequence 57042, A
Sequence 158280,
Sequence 158280,
Sequence 63329, A
Sequence 63329, A
Sequence 69610, A
Sequence 13412, A
Sequence 13412, A
Sequence 91, Appl
Sequence 91, Appl
Sequence 93596, A
Sequence 42100, A
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61 GC 	Match ocal S 8 564 1 51758	WS-11-121-086-61/c US-11-121-086-61/c Sequence 61, Application US/11121086 Publication No. US20050266459A1 GENERAL INFORMATION: APPLICANT: POULSEN, TIM S. APPLICANT: POULSEN, TIM S. APPLICANT: NUELSEN, KIRSTEN V. TITLE OF INVENTION: NUCLEIC ACID PR FILE REFERENCE: 09138.6000-00000 CCURRENT APPLICATION NUMBER: US/11/1 CURRENT FILING DATE: 2005-05-04 PRIOR FILING DATE: 2004-05-04 PRIOR APPLICATION NUMBER: 60/567,57 PRIOR FILING DATE: 2004-05-04 VIMBER OF SEQ ID NOS: 107 SOFTWARE: Patentin version 3.3 SEQ ID NO 61 LENGTH: 169495 TYPE: DNA CORGANISM: Homo sapiens FEATURE: NAME/KEY: modified base LOCATION: (70072)(70171) OTHER INFORMATION: a, c, g, t, unk FEATURE: NAME/KEY: modified base LOCATION: (139457)(157244) OTHER INFORMATION: a, c, g, t, unk US-11-121-086-61			մ ա ա ա Ֆ գ գ գ • • • • • ա ա ա ա գ գ գ գ գ գ գ գ գ	
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GGAGGGA          GGAGGGA	98. sy 99. srvative recercae	Cation US/11 120050266459A N: TIM S. N: TIM S. EN, KIRSTEN N: NUCLEIC A 001 000 000 ON NUMBER: U ON NUMBER: 60/: 12004-05-04 NOS: 107 n version 3.  apiens ed base ). (70171) N: a, C, 9, N: a, C, 9, N: a, C, 9,		200628 527 527 665 2508 509 514	6 18 18 12	1198 1198 1198 1198 1198 1133 1533 220895 201
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CTGGAGGCGAGGGAGCCTCCTGAGGCAGGGCAGGGCAGCCGTCAGGTGGGTG	Secre 53; DB 14; Length 1694 imilarity 99.8%; Pred. No. 1.4e-138; ; Conservative 0; Mismatches 0; Indels ; Congressive 0; Mismatches 0; Indels	1. 21D PROBES AND NUCLEIC ACID 300 3011/121,086 -04 567,570 3 3 3 4 7 7 7 7 8 8 7 8 8 8 8 8 8 8 8 8 8 8 8	ALIGNMENTS	US-01-121-086-62 US-09-925-065A-736106 US-09-925-065A-8136106 US-09-925-065A-813895 US-09-925-065A-726190 US-11-072-512-1958 US-09-925-065A-248642 US-09-925-065A-248643 US-09-925-065A-248643 US-10-301-480-328622	US-10-301-480-701461 US-10-301-480-701461 US-10-995-561-493 US-10-995-561-492 US-09-925-065A-918774 US-09-925-065A-919302 US-09-925-065A-917128 US-09-925-065A-917128	US-09-925-065A-42329 US-10-301-480-14356 US-10-301-480-73657 US-10-301-480-756975 US-10-301-480-756976 US-09-925-065A-685510 US-09-925-065A-685511 US-09-925-169-88 US-10-775-169-88 US-10-995-561-12594 US-10-995-561-12594
AGGTGGGTGACGGCA 120                 AGGTGGGTGACGGCA 51639	n 169495;  ls 1; Gaps 1;  ACTCACCCCATGTG 60                  ACTCACCCCCATGTG 51699	ANALOG PROBES		Sequence 62, Appl Sequence 736105, Sequence 736106, Sequence 813895, Sequence 726390, Sequence 1958, Ap Sequence 248642, Sequence 248643, Sequence 328622,	Sequence 88052, A Sequence 701461, Sequence 493, App Sequence 492, App Sequence 918774, Sequence 919302, Sequence 917128, Sequence 917128,	Sequence 42329, A Sequence 143566, Sequence 143567, Sequence 756975, Sequence 756976, Sequence 685510, Sequence 685511, Sequence 88, Appl Sequence 12574, A Sequence 12594, A

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APPLICANT: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
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US-09-925-065A-734471
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                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 734471
                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
-09-925-065A-734471
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/289,846 PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                               ENGTH: 541
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                                                                64 GGAGGCGAGGGAGCCTCCTGAGGCAGGGCCA 94
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                                                                                                                      GCCCTCCCTCGGAAACCAGGAAGGCTGGGCACCCTCCGTGGGCCTCACCCTCATTTGGAA 501
                                                                                                                                                              GCCCTGCCTCAGAAAACAGAAGGACGCAGCACACTCACGGTGACTCACCCCCATGTGGCT 63
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                                         TGATGAGAGGTGTTCCCCCAAGGCCTGGGCCA 532
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Pred. No. 0.64;
0; Mismatches 32;
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FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOCTWARE: PALEORIN Version 3.1
SEQ ID NO 32987
LENGTH: 712
TYPE: DNA
ORGANISM: Bovine 19866880739882
US-10-750-185-32987
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Sequence 20, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, TIM S.
APPLICANT: NIELSEN, TIM S.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG
FILE REFERENCE: 09138.6000-00000
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32987, Application US/10750185 Publication No. US20050260603A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
SEQ ID NO 20
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISS, SUE K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
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CURRENT FILING DATE: 2005-05-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCATGGGCAGGTGGGCAGGTCAGGCTGTGAGCACCTTCCCCAGAGCCAATGACCAAAAAT 145222
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RESULT 6
US-09-925-065A-57042/c
; Sequence 57042, Application US/09925065A
; Publication No. US20040181048A1
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; ORGANISM: Bovine
US-10-750-623-32987
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US-10-750-623-32987
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APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION UMBER: US 60/437,482
PRIOR APPLICATION WIMBER: US 60/437,482
SECOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
SEQ ID NO 32987
LENGTH: 712
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Best Local Similarity 47.6%;
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 32987, Application US/10750623 Publication No. US20050287531A1
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Best Local Similarity
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APPLICANT: DENISE, Sue !
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, DE
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                                                                                                                                                                                                                                                                                                                                                                               TCCCATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAACCAAGG 366
                                                                                                                  TGCCTCATCCTCTCTCCATTCTCCATAAGAGCCTCGGAAGAGACTG
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KERR, Richard
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ilarity 47.6%;
Conservative
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Pred. No. 3.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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US-10-301-480-158280/c
US-10-301-480-158280/c
; Sequence 158280, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
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                                                                                                                                                                                                                                                                              ; TYPE: DNA; Homo sapien; ORGANISM: Homo sapien US-10-301-480-158280
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-57042
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 158280
LENGTH: 1172
                                                                                                                                                                                     Matches
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4
                                                                                                                                                                                                             Local
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Local Similarity 59.8%;
  539
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al Similarity 59.8%;
61; Conservative
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                                           GGCAGGGCCAGGCAGCCGTCAGGTGGACGGCAGGGGTC 126
                                                                                                                    GGAAGGGAGAGCCAGCCAGCGAGGTGACAGGTGACATC
GGAAGGGAGAGCCAGCCAGCGAGGTGACAGGTGACATC
                                                                                           GGGGGCAGCCCTGGCATGGTGACTTTGGCAGATGGAGGAGAAGACACAGGAGCAGCGAGA
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                                                                                                                                                                                                           Score 36.4;
Pred. No. 6;
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Pred. No. 6;
                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                DB 9;
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                                                                                                                                                                                     41;
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Sequence 771689, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR TILING DATE: 2002-08-09
pRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 771689
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63329
LENGTH: 201
TYPE: DNA
ORGANISM: Homo Bapiens
US-10-995-561-63329
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US-10-95-561-63329/c
US-10-95-561-63329/c
; Sequence 63329, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
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RESULT 10
US-10-995-561-69610
; Sequence 69610, Application US/10995561
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; ORGANISM: Homo sapien
US-10-301-480-771689
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US-10-301-480-771689/c
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Best Local Similarity
Matches 64; Conserv
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Best Local Similarity 59.8%;
Matches 61; Conservative
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: CL001559
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                                                                                                                                                                                                            85 GGCAGGGCCAGGGCAGCCGTCAGGTGGGTGACGGCAGGGGTC 126
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                                                                                                                  TGGGTGCGGGTGGGCTGGCTCCTGCCATCAGGCGCACGGTGGCTTCATGCAG 26
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                                                                                                                                                                                                                                                                                              6.3%; Score 35.8; DB 8; Length 2 ilarity 56.6%; Pred. No. 6.5; Conservative 1; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36.4; DB 10; Length 1172; Pred. No. 6; 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                               DB 8; Length 201;
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RESULT US-10-1 Seque Publ: GENE: App: TIT! TIT! FILL FILL FILL FILL FILL FILL FILL	B 8	D Q	Que:	; SEQ ; LI ; OI ; OI	ser con	THE	RESULT US-10-9 ; Seque ; Publ:	B &	B &	Quer Best Matcl	; EI ; CUI ; NUI ; SOI ; SEQ ; LI ; TY ; OI US-10.	GENI GENI API TII
SULT 12 -10-995-561-13364/c Sequence 13364, Application US/10995561 Sequence 13364, OUS20050272054A1 SUBJECT OF US20050272054A1 GENERAL INFORMATION: APPLICANT: CARGILL, Michele et al. TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS TITLE OF INVENTION: DETECTION AND USES THEREOF FILE REFERENCE: CL001559	105 CAGGTGGGTGACGGCAGGGGTCTTGCCATGGTGGGCACAGGGGCTGCATACAG 157	45 GACTCACCCCATGTGGCTGGAGGCGAGGGAGGCCCCCCCC	Query Match 6.3%; Score 35.8; DB 8; Length 25257; Best Local Similarity 56.6%; Pred. No. 15; Marches 64: Conservative 1: Mismatches 48: Indels 0: Gaps	ID NO 13412 INGTH: 25257 PEE: DNA GANISM: Homo sapiens	CURRENT APPLICATION NUMBER: US/10/995,561 CURRENT FILING DATE: 2004-11-24 NUMBER OF SEQ ID NOS: 85702 SOFTWARE: FastSEQ for Windows Version 4.0	APPLICANT: CARGILL, Michele et al. TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS TITLE OF INVENTION: DETECTION AND USES THEREOF	SULT 11 -10-995-561-13412 Sequence 13412, Application US/10995561 Publication No. US20050272054A1 GRNERAL INFORMATION:	105 CAGGTGGGTGACGGCAGGGGTCTTGCCATGGTGGGCACAGGGGGTGCATACAG 157	45 GACTCACCCCCATGTGGCTGGAGGCAAGGGAGCCTCCTGAGGCAGGGCAGGGCAGCCGT	Query Match 6.3%; Score 35.8; DB 8; Length 201; Best Local Similarity 56.6%; Pred. No. 6.5; Matches 64; Conservative 1; Mismatches 48; Indels 0; Gaps	REENT APPLICATION RRENT PILING DATE WHER OF SEQ ID NOS FYMARE: FASTSEQ fo ID NO 69610 SEGTH: 201 SEGTH: DNA YEE: DNA RGANISM: Homo sapi	Publication No. US20050272054A1  GENERAL INFORMATION: APPLICANT: CARGILL, Michele et al. TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS TITLE OF INVENTION: DETECTION AND USES THEREOF
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RESULT 14
US-10-301-480-93596/c
J Sequence 93596, Application US/10301480
J Publication No. US20060057564A1
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; ORGANISM: Homo sapiens
US-11-121-086-91
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US-11-121-086-91/c
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Best Local Similarity 51.5%;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OP INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG
FILE REFERENCE: 99138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR PILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
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CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
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OTHER INFORMATION: n = A,T,C or G,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature LOCATION: (1)...(86361
                                                                                                                                                                                                                                                   3
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                                                                                                                                                                                                                                                                                               362 CAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                            106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
                                                                                                                                           G-CACTGCCCGCCGCCTCTGCGATGC 506
                                                                                                                                                                                     CCTGAGCATTGGGCCTCCCCTTTCTCTTCCCCAGACCCCTGGACATGCCCTTGGCGGCAA 107300
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                                                                                                                 GTCCCTGCACACCTGCTCTGTGCAGC 107274
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56.6%;
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Pred. No. 23;
0; Mismatches
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Pred. No. 18
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CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FRABLSEQ for Windows Version 4.0
SEQ ID NO 93596
LENGTH: 1741
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US-10-301-480-707005/c
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                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: In the Human Genome

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 10/215,598

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 707005

LENGTH: 1741
                                                                                                                                                                                                                             Query Match
Best Local S
Matches 80
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Best Local Similarity 51.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapien
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                     192
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                                                                                                                                                                                    72
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CTCTGGAAGTCTGGAAGTGAGCAATGTTTCCCATT 226
                                                               AGAGCCTTCAGGGGAGCATGGTCCTGCTGACATCTTGACTGCAGACATCTGGCTTCCAGA
                                                                                                   ATGGTGGGCACAGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCCCTGGTGCCAGC 191
                                                                                                                                             GGGATGATGCTGACACAGGGAGCGTGGAGGGGCTGGGAGAGGCAGGGAAGGGTCCTCCCC
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Pred. No. 15;
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18:31:06	70 GTATGACAGAGTGCATTTCGGTGAAGTCGCCCAGT 36
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Maximum Match 100%
Listing first 45 summaries
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1: /SIDSS/ptodata/1/pubpna/USO8 NEW_PUB.seq:*

2: /SIDSS/ptodata/1/pubpna/USO8 NEW_PUB.seq:*

3: /SIDSS/ptodata/1/pubpna/USO7 NEW_PUB.seq:*

4: /SIDSS/ptodata/1/pubpna/USO9 NEW_PUB.seq:*

5: /SIDSS/ptodata/1/pubpna/USO9 NEW_PUB.seq:*

6: /SIDSS/ptodata/1/pubpna/USO9 NEW_PUB.seq:*

7: /SIDSS/ptodata/1/pubpna/USO1 NEW_PUB.seq:*

8: /SIDSS/ptodata/1/pubpna/USO1 NEW_PUB.seq:*

9: /SIDSS/ptodata/1/pubpna/USO1 NEW_PUB.seq:*

10: /SIDSS/ptodata/1/pubpna/USO1 NEW_PUB.seq:*

11: /SIDSS/ptodata/1/pubpna/USO1 NEW_PUB.seq:*

12: /SIDSS/ptodata/1/pubpna/USO1 NEW_PUB.seq:*

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14: /SIDSS/ptodata/1/pubpna/USO1 NEW_PUB.seq:*

15: /SIDSS/ptodata/1/pubpna/USO1 NEW_PUB.seq:*

16: /SIDSS/ptodata/1/pubpna/USO1 NEW_PUB.seq:*

17: /SIDSS/ptodata/1/pubpna/USO1 NEW_PUB.seq:*

18: /SIDSS/ptodata/1/pubpna/USO1 NEW_PUB.seq:*
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Match Length
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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        gcagccctgcctcagaaaac.....agtggcgtctttcggacttc
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  5 14 US-11-121-086-61

16 US-09-925-065A-734471

9 14 US-11-121-086-20

18 US-10-750-185-39987

18 US-10-750-623-32987

18 US-10-95-561-63329

19 US-10-995-561-63329

10 US-10-995-561-13412

10 US-10-995-561-13412

10 US-10-995-561-1364

10 US-10-995-561-1364

10 US-10-301-480-707005

10 US-10-301-480-707005

10 US-10-750-623-42100

10 US-10-750-623-42100

10 US-10-301-480-716689

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10 US-10-301-480-7716689

10 US-10-301-480-7716689
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Biocceleration
Sequence 61, Appl
Sequence 734471,
Sequence 32,987, A
Sequence 32987, A
Sequence 63329, A
Sequence 63329, A
Sequence 13412, A
Sequence 13412, A
Sequence 13, Appl
Sequence 91, Appl
Sequence 93596, A
Sequence 93596, A
Sequence 42100, A
Sequence 42100, A
Sequence 57042, A
Sequence 57042, A
Sequence 158280,
Sequence 771689,
Sequence 42328, A
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	5.9	5.9	5.9	5.9	6.0	6.0	6.0	6.0		_	6.0	6.0	6.0	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.2	6.2	6.2	6.2	6.2	6.2	6.2
	514	509	509	2508	665	52,7	527	527	200628	169725	813	811	699	5232	5051	1926	1926	201	201	220895	1533	1533	1198	1198	1198	1198	1198
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AT.TONMENTS	US-10-301-480-328622	US-09-925-065A-248643	US-09-925-065A-248642	US-11-072-512-1958	US-09-925-065A-726390	US-09-925-065A-813895	US-09-925-065A-736106	US-09-925-065A-736105	US-11-121-086-62	US-11-121-086-63	US-09-925-065A-917128	US-09-925-065A-919302	US-09-925-065A-918774	US-10-995-561-492	US-10-995-561-493	US-10-301-480-701461	US-10-301-480-88052	US-10-995-561-12594	US-10-995-561-12574	US-10-775-169-88	US-09-925-065A-685511	US-09-925-065A-685510	US-10-301-480-756976	US-10-301-480-756975	US-10-301-480-143567	US-10-301-480-143566	US-09-925-065A-42329
	Sequence 328622,	Sequence 248643,	•	Sequence 1958, Ap	Sequence 726390,	Sequence 813895,		Sequence 736105,	Sequence 62, Appl	Sequence 63, Appl		Sequence 919302,			Sequence 493, App		88052,	12594,		Sequence 88, Appl	Sequence 685511,	Sequence 685510,		Sequence 756975,	Sequence 143567,	Sequence 143566,	Sequence 42329, A

## ALIGNMENTS

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Sequence 61, Application US/11121086

Sequence 61, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PatentIn version 3.3

SEQ ID NO 61

TENTORY FILING DATE: 1004-05-04
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                                                                                                                                                                                                                                                               LENGTH: 169495

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified base
LOCATION: (70072)...(70171)
OTHER INFORMATION: a, c, g, t, unknown or
FEATURE:
                                                                                                                              Query Match 97.8%;
Best Local Similarity 99.6%;
Matches 563; Conservative
                                                                                                                                                                                                            NAME/KEY: modified base LOCATION: (139457) (157244) OTHER INFORMATION: a, c, g,
                                                                51758
51698
                 t, unknown
                                                                                                                            Score 551.4; DB 14;
Pred. No. 1.6e-137;
0; Mismatches 1;
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US-09-925-065A-734471
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                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-734471
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILLING DATE: 2000-11-20
PRIOR PELICATION NUMBER: US 60/250,092
PRIOR FILLING DATE: 2000-11-30
PRIOR FILLING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILLING DATE: 2001-01-16
PRIOR PELICATION NUMBER: US 60/289,846
PRIOR FILLING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 734471, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT PILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ
SEQ ID NO 734471
                                                                                                                                                                                                                                                                                                                                               LENGTH: 541
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                                                                             64 GGAGGTGAGGGAGGCCTCCTGAGGCAGGGCCA 94
                                                                                                                                                               4 GCCCTGCCTCAGAAAACAGAAGGACGCAGCACTCACGGTGACTCACCCCCATGTGGCT 63
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                                         TGATGAGAGGTGTTCCCCCAAGGCCTGGGCCA 532
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                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                      7.1%;
64.8%;
                                                                                                                                                                                                   ; Score 39.8; DB; Pred. No. 0.7; 0; Mismatches
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Sequence 20, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRGTEN V.
FILLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 05/504
SPRIOR APPLICATION NUMBER: 05/504
SPRIOR APPLICATION NUMBER: 05/507,570

PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.3
SEQ ID NO 20
LENGTH: 162289
                                                                 APPLICANT: DeNISE, Sue K.

APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOY
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOPTWARE: PATENTIN VERSION 3.1
SEQ ID NO 32987
LENGTH: 712
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; ORGANISM: Homo sapiens
US-11-121-086-20
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US-11-121-086-20/c
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-32987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 32987, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.0%;
Best Local Similarity 46.9%;
Matches 123; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGCCATGCCCCCCAACGTTGC 264
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                            19866880739882
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Pred. No. 2.1;
0; Mismatches 139;
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RESULT 6
US-10-995-561-63329/c
; Sequence 63329, Application US/10995561
; Publication No. US20050272054A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Bovine
US-10-750-623-32987
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US-10-750-623-32987
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.6%; Score 37; Best Local Similarity 47.6%; Pred. No. Matches 109; Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32987, Application US/10750623 Publication No. US20050287531A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING
FILE REFERENCE: MMI1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MMI.GENOMICS,
APPLICANT: DeNISE, Sue F
APPLICANT: KERR, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 712
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                                                                                                                                                                                                                                                                                   GAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGAGGGTGGGGCTGG
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KERR, Richard
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47.6%;
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Pred. No. 4.1;
0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  ed. No. 4.1;
Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 8; Length 712;
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APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONDENTIALS OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 63329

LENGTH: 201

TYPE: DNO 63329

LENGTH: 201
RESULT 8
US-10-995-561-13412
(Sequence 13412, Application US/10995561)
; Sequence 13412, Application US/10995561
; Publication No. US20050272054A1
; Publication No. US20050272054A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
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US-10-995-561-69610
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FBSTSEQ for Windows Version 4.0
SEQ ID NO 69610
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Best Local S
Matches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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Publication No. US20050272054A1
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                105 CAGGTGGGTGACGGCAGGGGTCTTGCCATGGTGGGCACAGGGGCTGCATACAG 157
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Similarity 56.6%;
64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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Pred. No. 6.9;
1; Mismatches
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RESULT 10

US-11-121-086-91/c

Sequence 91, Application US/11121086

Sequence 91, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:

APPLICANT: NIELSEN, TIM S.

APPLICANT: NIELSEN, TIM S.

TITLE OF INVENTION: NUCLBIC ACID PROBES AND NUCLBIC ACID ANALOG:

FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/21,086

CURRENT FILING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR FILING DATE: 2004-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(86361)
OTHER INFORMATION: n = A,T,C or G,
US-10-995-561-13364
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; ORGANISM: Homo sapiens
US-10-995-561-13412
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US-10-995-561-13364/c
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Best Local S
Matches 64
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CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13364
LENGTH: 86361
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Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE,
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOUISS9
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NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 13412
LENGTH: 25257
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Pred. No. 16
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Pred. No. 1
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RESULT 11
US-10-301-480-93596/c
; Sequence 93596, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
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US-10-301-480-93596
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; ORGANISM: Homo
US-11-121-086-91
                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: PastSEQ for Windows Version 4.
SEQ ID NO 93596
LENGTH: 1741
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Best Local Similarity
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TITLE OF INVENTION: Identifiction and Mapping
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 10/215,598 PRIOR FILING DATE: 2002-08-09
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                                                                                                                                                                                                                Match 6.2%;
Local Similarity 51.6%;
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 GTATGACAGAGTGCATTTCGGTGAAGTCGCCCAGT
                                                               AGAGCCTTCAGGGGAGCATGGTCCTGCTGACATCTTGACTGCAGACATCTGGCTTCCAGA
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Pred. No. 25;
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RESULT 12 US-10-301-480-707005/c ; Sequence 707005, Application US/10301480 ; Publication No. US20060057564A1 ; GENERAL INFORMATION:

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; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-42100
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US-10-301-480-707005
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 42100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 42100, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
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Best Local :
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
FILE OF INVENTION: in the Human Genome
FILE REFERENCE: 108027.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
FRIOR APPLICATION NUMBER: US 10/215,598
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
NUMBER OF SEQ ID NOS: 1226818
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, David G.
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                                                                                                                                                                  Match 6.2%;
Local Similarity 50.6%;
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Pred. No. 16;
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CURRENT APPLICATION NUMBER: US/10/750,623;
CURRENT FILING DATE: 2003-12-31;
PRIOR APPLICATION NUMBER: US 60/437,482;
PRIOR FILING DATE: 2002-12-31;
NUMBER OF SEQ ID NOS: 64922;
SOFTWARE: PatentIN version 3.1;
SEQ ID NO 42100
LENGTH: 835
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; ORGANISM: Bovine
US-10-750-623-42100
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                                                                                                                                                                       Sequence 57042, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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Best Local (
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-1
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BATES, Stephen
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0; Mismatches
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILLING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILLING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILLING DATE: 2001-01-16
PRIOR FILLING DATE: 2001-05-09
PRIOR FILLING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 57042 LENGTH: 1172

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Minimum
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Maximum Match 100%
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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US-10-027-632-142126
US-10-027-632-142126
US-10-122-281-642
US-09-925-065A-734471
US-10-110-155-10
US-10-146-731-10
US-10-141-761-10
US-10-142-885-10
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US-10-143-895-10
US-10-141-755-10
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Sequence 142127,
Sequence 142126,
Sequence 142126,
Sequence 642, App
Sequence 6734471,
Sequence 734471,
Sequence 10, Appl
Sequence 1311, Ap
Sequence 1311, Ap
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	sequence
685511,	685510,	42329, A	42328, A	57042, A	3312, Ap	1312, Ap	10143, A	1312, Ap	258790,	258790,	11, Appl	11, Appl	11, Appl	12287, 4	52013, A	17803, A	5702, Ap	60160, A	20932, A	<ol> <li>Appli</li> </ol>	TALL, AP

## ALIGNMENTS

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Sequence 1. Application US/10798652
Publication No. US20040219582A1
GENERAL INFORMATION:
APPLICANT: Yongjun Guo
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISM IN THE
TITLE OF INVENTION: FGF-3 GENE AND METHODS OF USE THEREOF
FILLE REFERENCE: 3382-PO3136US01
CURRENT APPLICATION NUMBER: US/10/798,652
CURRENT FILING DATE: 2004-03-11
PRIOR APPLICATION NUMBER: 60/455,698
PRIOR APPLICATION NUMBER: 60/455,698
PRIOR PILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ FOR Windows Version 3.0
SEQ ID NO 1
LENGTH: 564
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAMES/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: n is cytosine or thymine
US-10-798-652-1
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Best Local Similarity
Matches 563; Conserv
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241 GCCGGCCATGCCCCCAACGTTGCACACTCACTGCCTTTTGCAGGGTTTGGGGCCTTCCAGTC
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                                                                                                                     GGGGTCTTGCCATGGTGGGCACAGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCC
                                                                                                                                                                                       CTGGTGCCAGCCTCTGGAAGTCTGGAAGTGAGCAATGTTTCCCATTAAGGAAAGTGTGTG
                                                                                                   GGGGTCTTGCCATGGTGGGCACAGGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCC
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Pred. No. 3e-164;
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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US-10-027-632-142127
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; ORGANISM: Human
US-10-027-632-142127
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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Best Local Similarity
Matches 562; Conserv
                                                                                                         167
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                                                                                                      GGCTGGGCTGGGCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCC
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  GGGGTCTTGCCATGGTGGGCACAGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCC
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                                                                                                                                                                                                                                                                                                                                                    Score 562; DB 5; 1
Pred. No. 6.4e-164;
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; ORGANISM: Human
US-10-027-632-142127
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US-10-027-632-142127
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ
SEQ ID NO 142127
LENGTH: 700
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Publication No. US20030204075A9
GENERAL INFORMATION:
                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                   Matches 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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                                                                                                                                   Conservative
                                                                                                                                                 99.6%;
                                                                                                                                  ۲.
                                                                                                                                  Score 562; DB 6;
Pred. No. 6.4e-164;
1; Mismatches 1;
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                                                                                                                                                                 Length 700
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,63
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
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                                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-142126
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                                                                                                                                                                                         SEQ ID NO 142126
LENGTH: 855
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                                                                               Query Match
Best Local
                                                           Matches
                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows
                                                         Local Similarity
es 563; Conserv
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                                                         Conservative
                                                                         98.0%;
                                                       Score 552.6; DB 5;
Pred. No. 5.4e-161;
1; Mismatches 0;
                                                                                                                                                                                                                                 Version
                                                         Indels
                                                                                          Length
                                                                                            855,
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                                   ; LENGTH: 855
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-142126
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GENERAL INVUKTALLAW:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 10827.129

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 
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US-10-027-632-142126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 142126, Application US/10027632 ; Publication No. US20030204075A9 ; GENERAL INFORMATION:
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APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in
FILE REFERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 642
LENGTH: 29340
TYPE: DNA
ORGANISM: Homo sapiens
US-10-322-281-642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-10-322-281-642
                                                                                                                          Query Match
Best Local S
Matches 563
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1; Mismatches 0;
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Pred. No. 2.1e-160;
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                                                                                                                                                                             ; ORGANISM: Homo sapiens US-09-925-065A-734471
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                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR PELICATION NUMBER: US 60/261,766
PRIOR PRILING DATE: 2001-01-16
PRIOR PELICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 734471
LENGTH: 541
TYPE: DNA
                                                                                                        Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 734471, Application US/09925065A Publication No. US20050228172A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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   GGAGGTGAGGGAGCCTCCTGAGGCAGGGCCA
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                                                                                                      7.1%;
nilarity 64.8%;
Conservative
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                                                                                                        Score 39.8; DB Pred. No. 0.062; O; Mismatches
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US-10-123-155-10
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APPLICANT: Beresini, Mauree
APPLICANT: Desroye, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Eller
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Applica publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A0106
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                                                   APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 933081C30
CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
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103; Conserv
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Watanabe, Colin K
Wood, William
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                                                                                                                                                                                                 Stewart, Timothy A.
                                                                                                                                                                                                                 Smith, Victoria
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o. US20040005560A1
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ilarity 48.8%;
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APPLICANT:

APPLICANT: APPLICANT: APPLICANT:

Tumas, Daniel Watanabe, Colin K Wood, William Zhang, Zemin

APPLICANT:

Stewart, Timothy A. Smith, Victoria

FILE REFERENCE: P3330R1C323
CURRENT APPLICATION NUMBER: US/10/146,731
CURRENT FILING DATE: 2002-05-15

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME

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US-10-146-731-10
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Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                     GENERAL INFORMATION
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 APPLICANT:
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APPLICANT:
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TYPE: PR
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                                                                                                                                                                                                                                                                             PAREKLT 542
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                     Baker, Kevin P.
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                                            Gerritsen, Mary E
Goddard, Audrey
                                                                           Gao, Wei-Qiang
                                                                                                      Deforge, Laura
Desnoyers, Luc
                                                                                         Filvaroff, Ellen
                                                                                                                                       Beresini, Maureen
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k; Pred. No. 0.26;
176; Mismatches
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Sequence 10, Application US/10140
Publication No. US20030138888Al
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
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US-10-140-472-10
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Best Local S
Matches 34
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 10
LENGTH: 594
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ORGANISM: Homo Sapien
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T: Zhang, Zemin
INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                    Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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                                                                                                                                                                                                                                                                                                                  Application US/10140472
                                          Tumas, Daniel
Watanabe, Colin K
Wood, William
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Gerritsen, Mary E.
                                                                                                                                                                                                               Desnoyers, Luc
Filvaroff, Ellen
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; FILE REFERENCE: P333OR1C168
; CURRENT APPLICATION NUMBER: US/10/140,472
; CURRENT FILING DATE: 2002-05-06
; Prior Apploication removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; SEQ ID NO 10
; SEQ ID NO 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-472-10
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PAREKLT 542
                                 ATGCAGT 509
                                                                                                                                                                 CATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGGGGCTGGGCTGGGCAAGGCCACC
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                                                                  GDRYRRGGRGLRHHSSSRSRSSWSLSPSRSRSLTRSRSHSPSPSQSRSRSRSRSQSPSPS
                                                                                                  AGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCCAGCACTGCCCGGCCGCCTCTGCG
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Conservative 176;
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Pred. No. 0.26;
76; Mismatches 277;
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RESULT 12 US-10-141-761-10 Sequence 10, Application US/10141761
Publication No. US20030148432A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen APPLICANT:
APPLICANT:
APPLICANT: APPLICANT APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Goddard, Audrey Godowski, Paul J. Gurney, Austin L. Tumas, Daniel Watanabe, Colin K Wood, William Smith, Victoria Stewart, Timothy A. Gurney, Austin L. Sherwood, Steven Gerritsen, Mary E Gao, Wei-Qiang Desnoyers, Luc Filvaroff, Ellen DeForge, Laura

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RESULT 13
US-10-142-885-10
// Sequence 10, Application US/10142885
// Publication No. US20030157604A1
// GENERAL INFORMATION:
// APPLICANT: Baresini, Maureen
// APPLICANT: Beresini, Maureen
// APPLICANT: DeForge, Laura
// APPLICANT: Desmoyers, Luc
// APPLICANT: Desmoyers, Luc
// APPLICANT: Gao, Wei-Qiang
// APPLICANT: Gao, Wei-Qiang
// APPLICANT: Goddard, Audrey
// APPLICANT: Godowski, Paul J.
// APPLICANT: Godowski, Paul J.
// APPLICANT: Godowski, Paul J.
// APPLICANT: Gurney, Austin L.
// APPLICANT: Gurney, Austin L.
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 9330R1C198
CURRENT APPLICATION NUMBER: US/10/141,761
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 10
LENGTH: 594
TYPE: PRT
ORGANISM: Homo Sapien
US-10-141-761-10
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Matches 34
                 APPLICANT:
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             Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Stewart
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7.0%; [
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Pred. No. 0.26;
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RESULT 14 US-10-158-790-10

Sequence 10, Application US/10158790
Publication No. US20030180879A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Beresini, Maureen

DeForge,Laura

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Desnoyers, Luc Filvaroff, Ellen Gao, Wei-Qiang Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J.

Gurney, Austin

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Best Local S
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 10
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TYPE: PRT
ORGANISM: Homo
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C248
CURRENT APPLICATION NUMBER: US/10/142,885
CURRENT FILING DATE: 2002-05-10
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Sequence 10, Application US/10137871
Publication No. US20030207350A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 933081C448
CURRENT APPLICATION NUMBER: US/10/158,790
CURRENT FILING DATE: 2002-05-30
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DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Search completed: March 25, Job time : 682.5 secs

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US-10-137-871-10
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SEQ ID NO 10
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333071CL53
CURRENT APPLICATION NUMBER: US/10/137,871
CURRENT FILING DATE: 2002-05-03
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PAREKLT 542
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Gurney, Austin L.
Sherwood, Steven
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

16 38.8 C 17 38.8	16 38.8		15 39.6		c 13 39.6		11	10	9 39.8	8 40	C 7 40	c 6 40.2	5 41.4	C 4 43	c 3 551.4	c 2 551.4	1 560.8	No. Score M	Result Q	
6.9 215604	6.9 203106	6.9 184532	7.0 190018	7.0 142979	7.0 119613	7.1 233561	7.1 116039	7.1 111934	7.1 103034	7.1 230041	7.1 153129	7.1 320658	7.3 125020	7.6 125020	97.8 150214	97.8 150110	99.4 10777	Length	Query	40
		9 AC124345	14 AC148588	8 AC000029	8 AC138582		8 AC007362	8 AF281074		9 AC111047			8 AF429315	8 AF429315	8 AP006345	14 AC097722	8 HS11Q13RP	DB ID		
	AC021667 Mus muscu	AC124345 Mus muscu	AC148588 Pan trogl	AC000029 Homo sapi	AC138582 Pan trogl	AC159874 Bos tauru	AC007362 Homo sapi	AF281074 Homo sapi	AC067978 Homo sapi	AC111047 Mus muscu	AC163209 Mus muscu	AC145527 Atelerix	AF429315 Homo sapi	AF429315 Ното варі	AP006345 Homo sapi	AC097722 Homo sapi	Y12377 H.sapiens F	Description		

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6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.7	6.8	6.8		6.8		6.8	6.8
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## ALIGNMENTS

repeat	FEATURES Bource	COMMENT	PUBMED REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE	RESULT 1 HS11013RP LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="11" /map="qi3" /tissue_type="placenta" /cione_lib="lambda_D3, Clontech_cat#HL1067J_lot_1221" /germline /germline /germline /spt_family="MIR2"	ed se	CNRSURA1967, Institut Gustave-Roussy, 39 Rue Camille Desmoulins, 94805 Villejuif CEDEX, FRANCE The BamHI site at the 3' end of this sequence (nt 10772) corresponds to the BamHI site at the 5' end of the FGF-3/int-2 gene sequence (nt 1; X14445), as ascertained by sequencing through this site.	Lab. de Genetique	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  1 Djenabi,S., Brison,O., Galdemard,C. and Lavialle,C. Sequence analysis of the transcription control region upstream of the human FGF-3 gene	HS11Q13RP 10777 bp DNA linear PRI 02-MAR-2000 H.sapiens FGF/int-2 gene upstream flanking region. Y12377.1 GI:1934871 Y12377.1 GI:1934871 Alu repeat; FGF-3 gene; int-2 gene; Ll repeat; MIR repeat. Homo sapiens (human)

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                                  AC097722 150110 bp DNA linear Homo sapiens chromosome UNK clone RP11-186D19, WOR SEQUENCE, 9 unordered pieces.
AC097722 GI:18308824
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HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP sapiens (human) sapiens
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2605. .2752
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7417._.7568
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                                                                    misc_feature
                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: plasmid, 46%
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 147449 bases at least Q40
Consensus quality: 148626 bases at least Q30
Consensus quality: 148680 bases at least Q20
Insert size: 150429; sum-of-contigs
Quality coverage: 8.73 in Q20 bases; sgarose-fp
Quality coverage: 7.35 in Q20 bases; sum-of-contigs
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Waterston,R.H.
Direct Submission
Submitted (22-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jan 24, 2002 this sequence version replaced gi:16306472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; 54%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center code: WUGSC
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Unpublished
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:http://genome.wustl.edu/gsc/index.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in tribs requence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                /mol_type="genomic DN
/db_xref="taxon:9606"
/chromosome="UNK"
estimated_length=unknown/
                                         /note="assembly_name:Contig25"
                                                                                                                                                                                       organism="Homo sapiens"
                                                                                          clone="RP11-186D19"
                                                                                                                                                                                                                                   ocation/Qualifiers,
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4: gap of unknown length
8: contig of 5754 bp in length
9: contig of 4121 bp in length
9: contig of 421 bp in length
9: contig of 5273 bp in length
2: contig of 5273 bp in length
2: contig of 5380 bp in length
2: gap of unknown length
2: gap of unknown length
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8: gap of unknown length
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                                     GGCTGGGCTGGGCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCC
                                                                                      CCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGG
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                       GGCTGGGCTGGGCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCC
                                                                       CCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGG
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clone_end:SP6
vector_side:right"
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/note="assembly_name:Contig32
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/note="assembly_name:Contig26"
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104670. .104769
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68993. .69092
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104770. .150110
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14120. .19392
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14020. .14119
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24873. .24972
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Matches 563; Conserv
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Homo sapiens sequence.
AP006345
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On Aug 5, 2005 this sequence version replaced gi:48290861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens genomic DNA
published Only in Database (2003)
2 (bases 1 to 150214)
Hattori,M., Toyoda,A., Taylor,T.D.,
Totoki,Y. and Sakaki,Y.
Direct Submission
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              ACAGGGTCCCATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAA 360
                                                                                                                                           CTGGTGCCAGCCTCTGGAAGTCTGGAAGTGAGCAATGTTTCCCATTAAGGAAAGTGTGTG 240
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                                                                            GCCGGCCATGCCCCCAACGTTGCACACTCACTGCCTTTGCAGGGTTGGGGGCTTCCAGTC 300
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ACAGGGTCCCATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAA 85530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="11"
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/clone="RP11-186D19"
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Pred. No. 2.7e-120;
0; Mismatches 1;
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% 11 clone:RP11-186D19, complete
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1 (bases 1 to 125020)

1 (bases 2., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S. Holmes,S.E., O'Hearn,E., Fleisher,A., Stevanin,G., Brice,A., Ingersoll-Ashworth,R.G., Fleisher,A., Stevanin,G., Brice,A., Potter,N.T., Ross,C.A. and Margolis,R.L.

A repeat expansion in the gene encoding junctophilin-3 is associated with Huntington disease-like 2

Nat. Genet. 29 (4), 377-378 (2001)
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RF429315
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-OCT-2001) Psychiatry, Johns I
Institutions, 600 N. Wolfe St., Baltimore,
Location/Qualifiers
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Mammalla; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                                                                 /map="16q24.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's Disease-Like 2 (HDL2)"
complement (35581. .35746)
/rpt_type=tandem
              /translation="MSSGGRFNFDDGGSYCGGWEDGKAHGHGVCTGPKGQGEYTGSWS
HGFEVLGVYTWPSGNTYQGTWAQGKRHGIGLESKGKWVYKGEWTHGFKGRYGVRECAG
NGAKYEGTWSNGLQDGYGTETYSDG"
                                                                                                                                                                                                             complement (<36507. .>36887)
                                                                                                                    membrane and endoplasmic reticulum"
                                                                                                                                                                complement (<36507. .36887)
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol type="genomic DNA"
                                                           /protein_id="AAL40941.1"
/db_xref="GI:17646245"
                                                                                         /product="junctophilin 3"
                                                                                                                                  note="component of the junctional complex between
                                                                                                                                                                              /product="junctophilin 3"
                                                                                                                                                                                                                           /note="synonym:
                                                                                                                                                                                                                                         complement (<36507. .>36887)
/gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/chromosome="16"
                                                                                                      codon_start=1
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                                                                                                                     JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
AF429315
                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
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Best Local
                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                               TITLE
                                                                                                       JOURNAL
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/ Match 7.6%; Sco
Local Similarity 12.0%; Prones 64; Conservative 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17061 MSSYSYSGKYSWGMKSYMWRSYYSKRSTSKAWRSSKRGMGTGGRYKGGGRSY 17010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17541 MRSSKSSSWSMSMARSSWCMGWGAGYRRSKRSAGWGAGWRSSKGKRSTGMKRACSKKTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17421 MKKKGCTGYRGMSSKKSGYKSMRGMRGSSYSTSCWKSCWGYSWMKCMKYMSYKKKRRSMR 17362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AAGGACGCAGCACACTCACGGTGACTCACCCCCATGTGGCTGGAGGTGAGGGAGCCTCCT
                                                                                                                                                                                                                                                                                                                              1 (bases) to 125020)

1 (bases) to 125020)

1 (bases) to 125020

Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hw Ingersoll-Ashworth, R.G., Fleisher, A., Stevanin, G., Bric Potter, N.T., Ross, C.A. and Margolis, R.L.

A repeat expansion in the gene encoding junctophilin-3 associated with Huntington disease-like 2

Nat. Genet. 29 (4), 377-378 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens junctophilin 3 (JPH3)
                                                                                                                 2 (bases 1 to 125020)
Bolmes,S.E., Ingersoll-Ashworth,R.G., Ross,C.A. and Margolis,R.L.
Direct Submission
Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical
Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF429315.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRKGRKCMSSRKMKMYKSYYRRKRWMTCMKMCYSMYMAMYCRSMCCMCMCKSCCGCYSMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSMSSKGWRGYAGRGCYSSSMWSTRKRRSKCYSYKSYKKGRGKMKGWGGMKRGSKYWSSM 17302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCCCTGGTGCCAGCCTCTGGAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGCAGGGCCAGGCCAGCCGTCAGGTGGGTGACGGCAGGGGTCTTGCCATGGTGGGCAC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGATGCAGTCCTCCTGGCCACCTGAGAACAGCCTGTAGAGAGGCAGTGGCGT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCCAGCACTGCCCGCCGCCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGRMSSKSCYRSGTRRRCMKSKCRRGSRGKSMGMTRGRSGGKTSYSAKGSGRGCYYCWGW 17122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGGTGGGGCTGGGCTGGGCAAGGCCA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RMGKTGCNYMYRRSRAMMNGNAAAAGCTTCCCCANTNGGGGGAAAAAGGGCGSASRASCY 17182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCCAGGTGGCTGCAGAAGGT--CCCTCGCAGTCATGAAACCAAGGGAAGGCTTGGGAAAC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKMKRSSWSKCYSTKSYKSGRRKSKGWGRSTKSKAKSSMRMAGSKCTYGSSYWSNNRRNN 17242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCACACTCACTGCCTTTGCAGGGTTGGGGCTTCCAGTCACAGGGTCCCATCCACGTACCA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGSTGRSMKKKKGYSKYSRGMKGKKKTCYCMWKYYKYRKTSMCWWYYMKSWGYKRYKRCC
/mol_type="genomic DN
/db_xref="taxon:9606"
                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:17646244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 8
Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brice, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRI 18-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                      RESULT 6
AC145527/c
LOCUS
                                                                                                                                      SOURCE
                                                                                                                                                                                          ACCESSION
VERSION
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                                                                                                                                                                      CEYWORDS
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Best Local (
                                                                                                                       ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51806 MSWYSKSCYTYSCMRKMCWCWSCMYRSARCCTWRSWTSCYWYSRRSTGWWRSKGWGCWCY
                                                                                                                                                                                                                                                                                                                                                                                                                52106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51986 RYRWRKMCWGMWTRKSKGKSYSNSSWGWMWGKGTSYMCCASSYAMSCRKGMRSATSWGCC 52045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332
                                                                                                                                                                                                                                                                                                                                                                                                                                                            392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 CCAGGGCAGCCGTCAGGTGGGTGACGGCAGGGGTCTTGCCATGGTGGGCACAGGGGCTGC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 GCACACTCACGGTGACTCACCCCCATGTGGCTGGAGGTGAGGGAGCCTCCTGAGGCAGGG
                                                              HTG; HTGS PHASEI; HTGS DRAFT.

Atelerix albiventris (middle-African hedgehog)

Atelerix albiventris

Atelerix albiventris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost;

Eukaryota; Metazoa; Chordata; Insectivora; Erinaceidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45
                                                                                                                                                                                                                                                               AC145527

320658 bp DNA linear HTG 19-JUL Atelerix albiventris clone LB4-283G23, WORKING DRAFT SEQUENCE,
                   Mammalia; Eutheria; Laurasiatheria;
Erinaceinae; Atelerix.
1 (bases 1 to 320558)
                                                                                                                                                                                          AC145527
AC145527.1 GI:32996768
Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S.,
                                                                                                                                                                                                                                       unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 7.3%; Score 41.4;
Similarity 11.5%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSAYSCMYMSKACKSSYCAKRSGCYKKYMGSMYYSTGSRSMWYTSTYSYCMYMSMMWWSY 51805
                                                                                                                                                                                                                                                                                                                                                                                                                RGSMGKGSMTKKSKGTGKGMWGRGGSWGKS 52135
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCATGGCTTTGATTTAGTGAGAGGGTGGG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YMSYRSASWCWGSTGSMRSYKSTWRSCWSCMRGSMSYYSRMRGKGGCASWSCYRKKSKRK 52105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGCAGAAGGTCCCTCGCAGTCATGAAACCAAGGGAGGCTTGGGAAACCACATCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CMMRSYTTSCTCYYGCYCMWKGKYWKRRSSYKSCYKKKSMTKYSMRGMSCYRGSRYMYSY 51985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRSCCMSWKTGYCKGKKSWSMKCATTGMKSCARKSMSCYCGKMCRRASCWGCYKCMSMKT 51925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATACAGCTTACTCAGTGACAATCGAGTCCCTGGTGCCAGCCTCTGGAAGTCTGGAAGTGA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCCTTTGCAGGGTTGGGGCTTCCAGTCACAGGGTCCCATCCACGTACCAGCCCAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAATGTTTCCCATTAAGGAAAGTGTGTGGCCGGCCATGCCCCCCAACGTTGCACACTCA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="16q24.3; between D16S520 and WI-12410"
/note="isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="junctophilin 3"
/protein id="AAL40941.1"
/protein id="AAL40941.1"
/db_xref="01:17646245"
/translation="MSSGGRENFDDGGSYCGGWEDGKAHGHGVCTGFKGQGEYTGSWS
/translation="MSSGGRENFDDGGSYCGGWEDGKAHGHGVCTGFKGQGEYTGSWS
HGFEYLGVYTWPSGNTYQGTWAQGKHGIGLESKGKWYYKGEWTHGFKGRYGVRECAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="component of the junctional complex between plasma membrane and endoplasmic reticulum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonym: JP3"
complement(<36507. .>36887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGAKYEGTWSNGLQDGYGTETYSDG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="junctophilin 3"
complement(<36507. .36887)</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (35581. .35746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ement (<36507. .>36887)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 125020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
  Hosseini, R.,
                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Center Code: PGABERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Funding agent: Programs for Genomic Applications (NHLBI) if library name is LBI to LB4, please see website for a description: http://www-ged.lbl-gov/cheng/BAC.html
These libraries are available through the BACPAC Resources Center: http://www.chori.org/bacpac/libraryres.htm as LBNL-1 to LBNL-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Phrap version 0.990329.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 21 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         available at:
http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=SREBF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: Plasmid; pUC18 Chemistry: Dye-terminator Big Dye
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Mus musculus chromosome 3, clone RP24-11708, complete sequence.
AC163209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoplan, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Liu, A., Mabbitt, R., MacCearthy, M., Meldrim, J., Meneus, L., Mihova, T., Micol, R., Norbu, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., O'Iver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stubs, M., Talamas, J., Tesfaye, S., Theodore, J., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                            Direct Submission

AL Submitted (07-JUN-2005) Broad Institute of MIT and Harvard, 320

Charles Street, Cambridge, MA 02141, USA

CB 3 (bases 1 to 153129)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,

Alloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J.,

Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,

DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,

Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D.,

Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,

Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I.,

Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T.,

Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,

MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C.,

McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V.,

Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C.,

O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,

Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,

Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R.,

Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,

Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J.,

Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R.,

Direct Submission,

Direct Submission,

Direct Submission,
                                                                                                                                                                                                                      Charles Street, Cambridge, MA 02141, USA
On Aug 3, 2005 this sequence version replaced gi:67003668.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sclurograum.

1 (bases 1 to 153129)

Birren, B., Nusbaum, C. and Lander, E.

Birren, B., Chromosome 3, clone RP24-11708
                                                                                                                                                                                                                                                                                                                   Direct Submission Submitted (03-AUG-2005) Broad Institute of MIT and Harvard,
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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HTG.
                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
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  Center project name: L3292
Center clone name: 117_0_8
                                                Contact: sequence_submissions@broad.mit.edu
                                                                                                                                                 Center: Broad Institute of MIT and Harvard
                                                                                                   Web site: http://www-seq.wi.mit.edu
                                                                                                                             Center code: WIBR
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FEATURES

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                                                                                                                                                  /rpt_family=MLTLAO"

complement(17617. .19453)

/rpt_family="L1_MM"

18133. .18163
                                                  /rpt_family="MIR"
complement(20852. .21030)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                         /rpt_tamily=".......complement(16123. .16262)
/rpt_family="B3A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="(TTTTTG)n"
complement(21943. .22157)
                                                                                                                                                                                                                 /rpt_family="(TATATG)n"
complement(17311. .1761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="(TCTA)n" 6984. .7110
                                   /rpt_1
21915
                                                                                             /rpt_ta
20758
                                                                                                                                                                                                                                                                                                                                                                                                                               complement (15710. .15820)
/rpt family="L1MA4A"
complement (15823. .16050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="L1_MM" complement(15710...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (14517. .14746)
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="(TG)n"
complement(11051. .11261)
/rpt_family="B4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (9528. .9910)
/rpt_family="MT2B"
                                                                                                                         note="single clone coverage"
19454. .20704
                                                                                                                                                                                                                                                /rpt
16928
                                                                                                                                                                                                                                                                              /rpt_f
                                                                                                                                                                                                                                                                                                            /rpt_r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="(A)n"
2907. .13123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP24-11708"
/clone_lib="RPCI-24 Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _family="B4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _family="(GAA)n"
|. .5876
                                                                                                                                                                                                                                                                              family="(TATATG)n"
2. .16925
                                                                                                             family="L1"
                                                                                                                                                                                                                                                                                                                          _family="(TG)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                 family="L1MA4A"
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                                                                                                                                                                                                                                                                                                             .16856
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RESULT 8
AC111047
AC111047
LOCUS
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230041 bp DNA linear ROD 10-OCT-2003
DEFINITION Mus musculus chromosome 3, clone RP23-176H24, complete sequence.
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                                                                                                                                                         76120 GACÁGGAGCCAGGGGTGGAGCTAGGGTAGGAGGCÁGGGCGGGCCAGAGCAGAAGGCAGG
                                                                                                                                                                                                                   76180 ACAAAGTAGCTGCTGGGAGCCAGGGCAGGAGGCAGGGGCCAGGGCCAAGTGCAGGAGCCCAAG 76121
                                                                                                                           421
                                                                                                                                                                                   361 CCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGG 420
                                                                                                                                                                                                                                               GGCTGGGCTGGGCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGCAGG 468
                                                                                             GGCGGGGCCAGGCAGGCAGGGCAGAGCCAGGGCAGGAGGCAGG 76013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (29240. .29627)
/rpt family="IAPEY LTR"
complement (29660. .29993)
/rpt family="CRRID"
30197 .30223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="B1_MM"
30733..30785
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24051.
                                                                                                                                                                                                                                                                                                                                                                                    /rpt_fami
38402...3
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39152. .39203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fami.
26685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="(TG)n"
complement(31417. .31571)
/rpt_family="RSINE1"
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complement(30891..31095)
/rpt_family="MIR"
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complement(23405. .2387
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                                                                                                                                                                                                                                                                                                                                     /rpt_family="(TTA)n"
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38280. .38428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (33166.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="(GGGGA)n"
31130. .31168
/note="single clone coverage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (30926. .31037)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="(TCTCC)n"
25614. .25618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="L2"
complement(22732. .22787)
/rpt_family="L1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="B3"
22301. .22397
                                                                                                                                                                                                                                                                                                                                                                                                                                              'rpt_family="RMER6A"
18071. .38261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="single clone coverage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt_family="(TTTG)n"
8871. .28954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family="(TTTC)n"
                                                                                                                                                                                                                                                                                                                                                                                                                               family="B3A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ily="AT_rich"
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Exampringe, MA 02141, USA

A (bases 1 to 230041)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,

Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,

Boyuslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,

Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,

Diaz, J.S., Dodge, S., Dooley, K., Dorrisk, L., Erickson, J., Faro, S.,

Ferreira, P., FitzGerald, M., Gage, D., Galagan, D., Hagos, B.,

Hall, J., Horton, L., Hulme, W., Tilev, L., Johnson, R., Jones, C.,

Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,

Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,

Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,

Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,

Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,

Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,

Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,

O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Rachupka, A., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,

Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,

Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,

Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Direct Submission

Note of the property o
                                                                                                                        Submitted (10-OCT-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON OCt 10, 2003 this sequence version replaced gi:34495134. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (07-SEP-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Nusbaum, C. and Lander, E.
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Birren, B., Nusbaum, C.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Mus musculus chromosome 3, clone RP23-176H24
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Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 176_H_24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                   /rpt family="Zaphod"
complement(12702. .12858)
/rpt familv="no"
/rpt_family="(CAAT)n"
complement(14607. .14691)
/rpt_family="Lx9"
                                              14535.
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5564. .5568
/note="<30 qual SNGL region"
complement (5599. .6129)
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complement(5063. .5383)
/note="single clone coverage"</pre>
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/db_xref="taxon:10090"
/chromosome="3"
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lone_end:SP6"
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5. .9059
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                                                                                                                                                                                                                                    Local Similarity
                                                                21424
                                                                                                                21364 GACAGGAGCCAGGGTGGAGCTAGGGTAGGAGGCAGGGCGGGGCCAGAGCAGAGGCAGG
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                                                                                                                                        361 CCAAGGGAGGCTTGGGAAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGG 420
                                                                                                                                                                                           301 ACAGGGTCCCATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAA 360
                                                                                                                                                                                                                       88;
 AC067978
                                                                                       GGCTGGGCTGGGCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGCAGG 468
                                                                                                                                                                   ACAMAGTAGCTGCTGGGAGCCAGGGCAGGAGGCAGGGGCAGGGCCAGTGCAGGAGCCAAG 21363
                                                               GGCGGGGCCAGGCCAGGAGGCAGGGCAGGCCAGGGCAGGCAGGCAGG 21471
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20124.
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21517. .21672
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33334. .33515
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/rpt_family="B4"
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                                                                                                                                                                                                                                            Length 230041;
linear
HTG 03-JUL-2000
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JOURNAL REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Collins, S., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McHord, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Santos, R., Severy, P., Spencer, B., Roy, A., Santos, R., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Volang, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 103034)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 2, clone CTD-2350K7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 2 clone CTD-2350K7 map 2, WORKING DRAFT SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                        Center project name: L9518

Center clone name: 2350 K 7

Center clone name: 2350 K 7

Sequencing vector: M13, M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 95545 bases at least Q40

Consensus quality: 99446 bases at least Q20

Consensus quality: 100858 bases at least Q20

Insert size: 101634; sum-of-contigs

Quality coverage: 4.5 in Q20 bases; agarose-fp

Quality coverage: 4.4 in Q20 bases; sum-of-contigs
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                         NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
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       1586
1585: contig of 1585 bp in length 1685: gap of 100 bp
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8791. .8890
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8891. .116
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21396. .21495
                                                                                                         16006. .21395
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11785. .159
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11685. .11784
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84: contig of 2794 bp in length
/84: gap of 100 bp
905: contig of 4121 bp in length
/005: gap of 100 bp
1395: contig of 4391 bp in length
1495: gap of 100 bp
26164: gap of 100 bp
34912: contig of 8748 bp in length
35012: gap of 100 bp
46466: contig of 11454 bp in length
4556: gap of 100 bp
46566: gap of 100 bp
57082: gap of 100 bp
71308: contig of 14226 bp in length
57082: gap of 100 bp
71408: gap of 100 bp
86559: contig of 14226 bp in length
91408: gap of 100 bp
103034: contig of 16375 bp in length
86659: gap of 100 bp
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15906. .16005
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3251. .4742
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AF281074
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                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 111934)
Rossignol, M., Gagnon, M.L. and Klagsbrun, M.
Direct Submission
Submitted (21-JUN-2000) Surgical Research,
Longwood Ave, Boston, MA, 02115, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 111934)
Rossignol,M., Gagnon,M.L. and Klagsbrun,M.
Genomic organization of human neuropilin-1 and neuropilin-2 genes:
identification and distribution of splice variants and soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF281074 111934 bp DNA
Homo sapiens neuropilin 2 (NRP2) gene,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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<3518. .>111422
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86660. .103034
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/estimated_length=100
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46467. .46566
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/estimated_length=100
71409. .86559
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Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete cds,
                                                                                                                                                                                                                                                                                                                                                                                            Children's Hospital,
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, alternatively
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43995. .44150,46123. .46592,48101. .48256,60728. .60872,
63412. .63761,65955. .66099,6934. .70050,73043. .73183,
83879. .84141,85679. .85775,86988. .87023,96451. .>96731)
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KLLMVIREDQGGEWKHGRIILPSYDMEYQIVFEGVIGKGRSGEIAIDDIRISTDVPLE
NCMEPISAFAVDIPEIHEREGYEDEIDDEYEVDWSNSSSATSGSGAPSTDKEKSWLYT
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83879. .84141,85679. .85775,86988. .87008,108610. .108660,
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111118. .111422)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDPILITIIAMSSLGVLLGATCAGLLLYCTCSYSGLSSRSCTTLENYNFELYDGLKHK
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/note="receptor for VEGF165 and
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      518. .3590,17760. .17937,36403. .36584,42688. .42918,
.44150,46123. .46292,48101. .48256,60728. .60872,
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HRFRYAAKKTDHSITYKTSHYTNGAPLAVEFTLTIKLEQDRGSHC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCMEPISAFAGENFKGGTLLPGTEPTVDTVPMQPIPAYWYYVMAAGGAVLVLVSVALA
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43995. 44150,46123. 46292,48101. 48256,60728. 660872,
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83879. .84141,85679. .85775,86988. .87008,96451. .>96731)
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note="receptor for VEGF165 and semaphorins class3"
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Query Match
Best Local S
Matches 59
64
                                                   4
                                                                               59;
                                                                                            Similarity
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                                                                               Conservative
                                                                                         7.1%;
                                                                              0;
                                                                                          Score 39.8;
Pred. No. 36;
                                                                              Mismatches
                                                                                                        BB
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                                                                                                       Length 111934;
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REFERENCE
AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University, 4444 Forest Park Avenue, S (bases 1 to 116039)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116039 bp DNA HOMO Bapiens BAC clone RP11-150F11 from 2, AC007362 AC007362.4 GI:10801453 HTG.
                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
Department of Genetics, Wash: additional information about http://genome.wustl.edu
                 Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-APR-2005) Genome Sequencing (University School of Medicine, 4444 Forest MO 63108, USA
On Oct 14, 2000 this sequence version repla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-OCT-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-MAR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Submitted (15-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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3 (bases 1 to 116039)
Waterston, R.H.
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Submitted (23-APR-1999) Genome Sequencing Center, Washington
School of Medicine, 4444 Forest Park Parkway, St.
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Waterston, R.H.
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The sequence of Homo sapiens BAC clone RP11-150F11
                                                                                    MAPPING INFORMATION:
                                                                                                                              restriction digest.
                                                                                                                                                                                                                                                                                                        NOTICE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae, Homo.
1 (bases 1 to 116039)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rect Submission
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(bases 1 to 116039)
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(bases 1 to 116039)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oct 14, 2000 this sequence version replaced gi:9211352.
                                                                                                                                                                                                                                                                                                                                                                                       Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                    Center project name: H_NH0150F11
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Center
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St. Louis,
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t Park Parkway, St.
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Missouri 63108, USA
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                      sequence, see
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Matches
                          Query Match
Best Local
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                                                                                                                                                                                            misc_feature
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59,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The clone sequenced to the left is RP11-325M10, 200 base pair overlap; the clone sequenced to the right is RP11-394E1, 200 base pair overlap. Actual start of this clone is at base position 117994 of RP11-325M10; actual end is at base position 115845 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The RPCI-11 human BAC library was made from the blood of one donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Freng Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either Research Genetics, Inc. (http://www.resgen.com) or Pieter de and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE INFORMATION:
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                             Similarity
Conservative
                                                                                                                                                                                                                                           YPODY PSHONCEWIVY APEPNOKIVLNENDHFEIEKHDCKYDFIEIRDDSESADLLG
KHGGNIAPPTIISGSGMLYIRFTSDYAROGAGFSLRYEIFKTGSESCSKRFTSENGTI
ESPGFPEKYPHNLDCTFTILAKEKMEIILGFIIFDLEHDFLOVGEGDCKYDWLDIWDG
IPHVGFLIGKYCGTKTPSELASSTGILSLTFHTDMAVAKDGFSARYTLVHQEFLENFQ
CNVPLGMESGRIANEQISASSTYSDGRWTPQSRLHGDDNGWTPNLDSNKEYLQVDLR
FLTMLTAIATOGAISRETQNGYYKSYKLEVSTNGEDMWYRHGKNHKVFQANNDATE
VVLNKLHAPLLTRFVRIRCOWHYSGIALRELFEGCRVTDAPCSNKHGMLSGLIADSQI
SASSTQEYLWSPSAARLVSSRSGWFPRIPQAQDGEEWLQVDLGTPKTVKGVIIQGARG
GDSITAVBARAFVRKFKVSYSLNGKOWEYIQDFRTQOPKLFEGNWYYDTPDIRREDFI
PAQTVRVYPERWSPAAGIGMRLEVLGCDWTDSKPTVETLGFTVKSEETTTPYPTEEBAT
ECGENCSFEDDXDLQLPSGFRCNFDFLEEPCGWMYDHAKWLRTTWASSSSPNDRTFPD
DRNFLRLQSDSQREGQYARLISPVHLPRSPVCMEFQXQATGGRGVALQVVREASQES
KLLWVIREDGGGEWKHGRIILPSYDMEYQIVFEGVIGKGRSGEIAIDDIRISTDVPLE
KUMPTIGEDAGGEWKHGRIILPSYDMEYQIVFEGVIGKGRSGEIAIDDIRISTDVPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(14041...14113,28294...28471,46943...47124,53228...5:
54535...54690,56663...56802,58641...58796,71269...71413,
73953...74302,76496...766406,80475...80591,83585...83725,
94424...94686,96224...96320,97533...97553)
/gene="NRP2"
join(14041...14113,28294...28471,46943...47124,53228...53
54535...54690,56663...56832,58641...58796,71269...71413,
73953...74302,76496...76640,80475...80591,83585...83725,
94424....94686,96224...96320,97533...>97553)
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                                                                                                                                                                                                                         NCMEPISAFA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This gene was based on gi (4505458)
Continues as H_NH0394E01.1"
                                                                                                                                  /gene="NRP2"
/note="CpG_island (%GC=64.9, o/e=0.68,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /produčt="unknown"
/protein id="AAX93216.1"
/brotein id="AAX93216.1"
/branslation="MDMFPLTWVFLALYFSRHQVRGQPDPPCGGRLNSKDAGYITSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP11-150F11"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="NRP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="CpG_island (*GC=70.3, o/e=0.84, #CpGs=108)"
|4041. .97553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:9606"
chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Homo sapiens neuropilin 2 (NRP2), mRNA.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="NRP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2630. .13592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                       7.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type="genomic
0,
                          Score 39.8;
Pred. No. 3
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA"
                               36,
                                                       밁
32;
                                                       8;
                                                    Length 116039;
  Indels
                                                                                                                                        #CpGs=145) "
0;
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Gaps
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4 GCCCTGCCTCAGAAAACAGAAGGACGCAGCACCACTCACGGTGACCTCACCCCCATGTGGCT

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AUTHORS
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                                                                   Allen, C., Allen, H., Alsbrooks, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Alsbrooks, S., Allen, H., Baraken, M., Caderson, E., Cardenas, V., Carter, K., Cavazos, I., Cessar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, J., Checker, M., Dsonga, L., Davila, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, N., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Franser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Errandez, S., Falls, M., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gebregovy, J., Hasaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Horera, M., Guerra, M., Gebregovy, J., Hasaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Hasaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Hasaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Hasaland, W., Hamilton, C., Hamilton, C., Hamilton, K., Harvey, Y., Hasaland, W., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, K., Harvey, Y., Hasaland, W., Hamilton, C., Hamilt
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                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC15987
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*** SEQUENCING IN PROGRESS ***, 26
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project name: CH240-418
Center clone name: CH240-418
Center clone name: CH240-318
Center clone name: CH240-30;
Consensus quality: 226744 bases at least Q40
Consensus quality: 226422 bases at least Q30
Consensus quality: 229869 bases at least Q20
Estimated insert size: 229962; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
Consensus quality: Coverage: 6x in Q20 bases; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

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125598 TCTGGCAGGTCCCTCAGGGTCAGGTCTGCCAGGGTGGGGGGAC

125552

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/db_xref="taxon:9913"
/clone="CH240-5418"
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140341: contig of 3747 bp in length
140391: gap of 50 bp
141698: contig of 1307 bp in length
141748: gap of 50 bp
151343: contig of 9595 bp in length
151393: gap of 50 bp
154790: contig of 3397 bp in length
154840: gap of 50 bp
166899: contig of 12059 bp in length
16949: gap of 50 bp
172673: gap of 50 bp
172673: gap of 50 bp
185758: contig of 13085 bp in length
185808: gap of 50 bp
210193: gap of 50 bp
226003: contig of 15810 bp in length
226103: gap of unknown length
226103: gap of unknown length
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227773: gap of unknown length
229134: contig of 1361 bp in length
229234: gap of unknown length
230327: contig of 1093 bp in length
230427: gap of unknown length
230427: gap of unknown length
231641: contig of 1214 bp in length
231741: gap of unknown length
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4 (bases 1 to 119613)

Lau.C.C.Y. and Roe,B.A.

Direct Submission
Submitted (04-AUG-2005) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
OK 73019, USA
On Jul 23, 2005 this sequence version replaced gi:67514672.
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Lau.C.C.Y. and Roe,B.A.
Direct Submission
Submitted (23-JUL-2005) Department Of Chemistry And Biochemistry,
Submitted (73-JUL-2005) Department Of Chemistry And Biochemistry,
Su
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Lau,C.C.Y. and Roe,B.A.
Direct Submission
Submitted (10-JAN-2003) Department Of Chemistry And Biochemistry,
Submitted (10-JAN-2003) Department Of Chemistry And Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pan troglodytes clone rp43-21p1, AC138582
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The University Of Oklahoma
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Lau, C.C.Y. and Roe, B.A
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Similarity 46.9%;
                                                GGTGCCAGCCTCTGGAAGTCTGGAAGTGAGCAATGTTTCCCATTAAGGAAAGTGTGTGGC
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/mol type="genomic DNA"
/db xref="teaxon:9598"
/clone="rp43-21p1"
/clone_lib="RPCI - 43 Male Chimpanzee BAC Library"
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                                             Query Match
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Matches 123; Conserv
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                                                                                                                                                                                                                        Submitted (09-APR-2003) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman OK 73019, USA
On Sep 24, 1999 this sequence version replaced gi:5870976.
Because these overlapping clones came from different libraries.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (01-JUN-2000) Dep
The University Of Oklahoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-SEP-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Normar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roe, B.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OK 73019, USA
5 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (13-SEP-1999) Dep.
The University Of Oklahoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (21-OCT-1996) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens Chromosome Unpublished
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AC000029
AC000029.17 GI:5922087
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Wang, Z. and Roe, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OK 73019,
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Kim, U.-J. and Simon, M.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                              organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                           1. .142979
                                                                                                                                    map="22q11.2"
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                                                         7.0%;
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me 22q11.2
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oma, 620 Parrington Oval, Room 208, Norman
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BAC Clone 865e9 In GNAZ-BCR Region,
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                                                                         Length 142979;
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133180 AGCTCAGCAGCAACCTGCGGGAGGCCACCCTGCTGGCCTGGTGAGTGGGATCACAGGAGG
                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 137286: contig of 137286 bp in length
* 137387 145329: contig of 7943 bp in length
* 145330 145429: gap of unknown length
* 145330 19018: contig of 44589 bp in length.
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Direct Submission
Submitted (18-MAR-2004) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Department Of Chemistry
The University Of Oklahoma
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On Jul 23, 2005 this sequence version replaced gi:66473101
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1 (bases 1 to 190018)
Lau,C., Fujiyama,A. and Roe,B.A.
Pan troglodytes BAC Clone ptb-92f23
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Mammalia; Eutheria;
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Pan troglodytes clone ptb-94f23,
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/clone_lib="PTB Male Chimpanzee BAC Library"
137287. 137287 | 137287 | 137287 | 145330 | 145429
/estimated_length=unknown
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Minimum DB
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geneseqn2000s:*
geneseqn2001as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

19	c 18	17	c 16	15	c 14	c 13	c 12	11	10	9	80	7	о 6	ი თ	n 4	ω	N	<b>–</b>	Result No.
35	35	35.2	35.2	35.4	35.6	35.8	35.8	36	36.2	37.2	37.2	37.2	37.2	38.2	38.2	551.4	551.4	563	Score
6.2	6.2	6.2	6.2	6.3	6.3	6.3	6.3	6.4	6.4	6.6	6.6	6.6	6.6	6.8	6.8	97.8	97.8	99.8	Query
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ABL58452	ACH25075	ACL64141	ACL70503	AAS19511	ABV51994	ABQ90455	AAQ94044	ADQ56739	ADZ51725	ADB60580	AAL07453	ABK42424	ABK34393	ADM01893	ABX34807	ADZ13482	ABD33482	ADT97901	ID
Abl58452 Human pel	Ach25075 Human adu	Acl64141 M. xanthu	Acl70503 M. xanthu	Aas19511 Reference	Abv51994 Human pro	Abq90455 M. capsul	Aag94044 Human ALD	Adq56739 Novel can	Adz51725 FR-008 po	Adb60580 Connectiv	Aal07453 Human rep	Abk42424 Genomic s	Abk34393 Human cDN	Adm01893 Human cDN	Abx34807 Human mdd	Adz13482 Human can	Abd33482 Human can	Adt97901 Human fib	Description

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Add84538 121P1F1 v	0 ADD84538	ï	1028	6.0	34	40	
Ach71544 Human gen	2 ACH71544	12	593	6.0	34	39	
Abq81844 Bifidobac	ABQ81844	6	349980	6.1	34.2	38	
Adn60624 Human sec	2 ADN60624	12	756	6.1	34.2	37	
Adg78333 Human sec		12	756	6.1	34.2	36	
Acd18942 Novel hum	ACD18942	œ	756	6.1	34.2	35	
Aax85016 Human sec	AAX85016	N	756	6.1	34.2	34	
Abq88096 Human ost	ABQ88096	6	92638	6.1	34.4	ü	O
Adq39152 Human SNP	3 ADQ39152	13	5232	6.1	34.4	32	O
Adq39151 Human SNF	3 ADQ39151	<u>,,</u>	5051	6.1	34.4	31	ი
Adr52737 Drug ther	3 ADR52737	Н	220895	6.1	34.6	30	O
Abk84798 Human cDN	ABK84798	σ	220895	6.1	34.6	29	O
Aal38337 Complemen	AAL38337	σ	215980	6.1	34.6	28	ი
Aak79886 Human imm	AAK79886	4.	40742	6.1	34.6	27	U
Aak68089 Human imm	AAK68089	4	40742	6.1	34.6	26	ი
Abd33385 Human can	3 ABD33385	Н	76180	6.2	34.8	25	U
Adr62531 Cotton cD	3 ADR62531	بر	792	6.2	34.8	24	ი
Adb60581 Connectiv	ADB60581	9	1797	6.2	35	23	
Aal07455 Human rep	AAL07455	4.	1797	6.2	35	22	
Abk42425 Genomic s	ABK42425	4.	1797	6.2	35	21	
Adpass's numen Fer	Z AUF100/4		TOTO	0.6	ú	6	

ALIGNMENTS

Human; ds; fibroblast growth factor-3; FGF-3; promoter; SNP; single nucleotide polymorphism; cancer; oesophageal cancer; 5'UTR; breast cancer; ovarian cancer; prostate cancer; head and neck cancer; oesophageal squamous cell carcinoma. Homo sapiens. Human fibroblast growth factor (FGF)-3 promoter 5' 27-JAN-2005 ADT97901; ADT97901 standard; DNA; 564 BP (first entry) proximal region.

variation Location/Qualifiers replace(69,Y)
/\*tag= a /standard\_name= "Single nucleotide polymorphism"
/note= "This SNP is specifically claimed in claim

ο

# US2004219582-A1.

04-NOV-2004.

11-MAR-2004; 2004US-00798652

17-MAR-2003; 2003US-0455689P.

(GUOY/) GUO Y.

Guo Y;

WPI; 2004-794435/78.

Novel isolated nucleic acid molecule having single nucleotide polymorphism in upstream untranslated region of fibroblast growth factor-3 gene, useful for assessing related susceptibility of mammal to cancer. Claim 1; SEQ ID NO 1; 15pp; English.

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CC comprising a sequence complementary to ADT97901, a vector comprising the CC ADT97901 operably linked to a reporter gene, a host cell comprising the CC vector, detecting a SNP in the RGF-3 gene in a mammal (involves isolating CC a nucleic acid sample from the mammal, and determining whether a cytosine CC reporter of the mammal, and determining whether a cytosine CC the method (comprising a first oligonucleotide probe which anneals specifically with the target portion of the mammal's genome, where the CC quencher attached to its separate nucleotide residues and the target portion includes the nucleotide residue located at position 69 of ADT97901, and a pair of primers for amplifying a reference portion of the FGF-3 gene, where the reference portion includes the nucleotide residue coligonucleotide probe that can anneal with a target portion of a mammal's genome, where the target portion includes the nucleotide residue coligonucleotide probe that can anneal with a target portion of a mammal's genome, where the target portion includes the nucleotide residue located at position 69 of ADT97901. The method is useful for detecting SNP in FGF 3 gene in a mammal, preferably a human, and is also useful for assessing the relative susceptibility of a mammal to cancer (especially osophageal cancer), which shows an association with the presence of the C-allele. CC ancer is chosen from osophageal cancer is osophageal squamous cell coffice fethylater for the factor (FGFP). The assessing the presence of the C-allele of fethylater for the factor (FGFP) and a marman untranslated region (UTR) of fethylater for the factor (FGFP).
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 564 BP; 117 A; 160 C; 185 G; 101 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule comprising tupstream untranslated region (UTR) of fibroblast growth factor (FGF)-3 gene sequence (ADT97901) with a single nucleotide polymorphism (SNP)at position 69. Also included are an isolated nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibroblast growth factor (FGF) - 3 gene sequence.
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                                                                                                                                                                    GGCTGGGCTGGGCAAGGCCACCAGGTCTGAGTCAGAGGCAAGAGGCAGGAAGCTGGTCCCC
                                                                                                                                                                                                                                                                                                 CCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGTCTTGCCATGGTGGGCACAGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCC
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AGCACTGCCCGCCCTCTGCGATGCAGTCCTCCTGGCCACCTGAGAACAGCCTGTAGAG
                                                                                                                             GGCTGGGCTGGGCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCC
                                                                                                                                                                                                                                                       CCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.8%;
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AGGCAGTGGCGTCTTTCGGACTTC

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CTGGTGCCAGCCTCTGGAAGTCTGGAAGTGAGCAATGTTTCCCCATTAAGGAAAGTGTGTG 240

GGGGTCTTGCCATGGTGGGCACAGGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCC 180 

GGGGTCTTGCCATGGTGGGCACAGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCC

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RESULT 2
ABD33482
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                                                                                                                                                                                                                                  The invention relates to cancer-associated proteins (CAP) and the cancer-cassociated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an continuous control of the partial cancer inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer drug candidate and monitoring the effect of the anticancer drug candidate on expression of the CA gene. The CAP proteins are useful for detecting concer associated with expression of a CAP protein in a test cell sample and for screening for a bioactive agent capable of modulating the cancer, involving determining the expression of a CA nucleic acid in a concer, involving determining the expression of a CA nucleic acid in a concer, involving determining the expression of a CA nucleic acid in a concer, involving determining the expression of a CA nucleic acid in a concer, involving determining the expression of a CA nucleic acid in a concer, involving determining the expression of a CA nucleic acid in a concern this sequence represents a human CA gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                      Matches 563;
                                                                                                          Query Match
Best Local
                                                                                                                                                                         Sequence 29340 BP; 6351 A; 8588 C; 8017 G; 6384 T; 0 U; 0 Other;
                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; SEQ ID NO 642; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human cancer associated protein encoded within open reading frame of cancer associated gene, useful as targets for diagnosing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morris DW, Malandro MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer-associated (CA) gene HD07-093.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAGR-) SAGRES DISCOVERY INC
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  3566 GCAGCCCTGCCTCAGAAAACAGAAGGACGCAGCACTCACGGTGACTCACCCCCATGTG
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                        1 GCAGCCCTGCCTCAGAAAACAGAAGGACGCAGCACACTCACGGTGACTCACCCCCCATGTG
                                                                                                              Similarity
                                                                                      Conservative
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                                                                                                          99.6%;
                                                                                                                                 97.8%;
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                                                                                        Pred. No. 9.3
0; Mismatches
                                                                                                            Score 551.4; DB 13; Pred. No. 9.3e-139;
                                                                                      Indels
                                                                                                                              Length 29340;
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                                                                                        Gaps
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RESULT 3
ADZ13482
ID ADZ1
XX ADZ1
XX ADZ1
XX D1ag
XX D1ag
XX D1ag
XX Cytc
XX D1ag
XX Cytc
XX D1ag
XX O7-J
XX CYC
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XX W21
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The invention relates to a nucleic acid array for detecting a cancer associated (CA) nucleic acid, comprising two or more nucleic acid probes. The invention also relates to a peptide array comprising two or more isolated polypeptides encoded by a CA nucleic acid sequence, a compound that binds to a polypeptide, an isolated antibody or its fragment which binds to a polypeptide, which is prepared by immunizing a host animal with a composition comprising the polypeptide or its antigen binding fragment and collecting cells from the host expressing antibodies against the antigen or its antigen binding fragment, a composition comprising the antibody and a carrier, a method of screening for anticancer activity, a method of detecting a CA nucleic acid, a method of diagnosing cancer, a
                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid array useful for detecting cancer
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SEXEXEXEX

ABX34807

standard; cDNA; 2161

ВP

Human mddt

CDNA SEQ ID 368

(first

MDDT; human; disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; osteopathic; cytostatic; ant

anti-HIV;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57501 BP; 13274 A; 15989
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GAGGCAGTGGCGTCTTTCGGACTTC 4280
                                                                                                                        GGCTGGGCTGGGCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCC
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Pred. No. 1.1e-138;
0; Mismatches 1;
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                                                                                                                                                                                                                             This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic, antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides and the polypeptides of the invention can be used for gene therapy, protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polynucleotides are particularly useful for diagnosing, treating or preventing cell purliferative disorders (e.g. cancers including adenocarcinoma, lukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis. ABX3440-ABX34835 encode the MDDT polypeptides represented in ABU11450-ABU11845, described in the disclosure of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                              Matches 103;
                                                                                                                                             Query Match
Best Local
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29-MAR-2001; 2001US-0280068P.
16-MAY-2001; 2001US-0291280P.
17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-0299428P.
20-JUN-2001; 2001US-0299776P.
20-JUN-2001; 2001US-0300001P.
                                                                                                                                                                                                 Sequence 2161 BP; 354 A; 658 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified disease detection and treatment molecule proteins polynucleotides, useful for diagnosing, treating or preventing (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, oste or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   haemostatio; nephrotropic; antianaemic; antipsoriatio; hepatotropic; gene therapy; protein replacement therapy; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 368; 339pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Daffo A, Jones AL, Tran AB, Dahl CR, Gie Dufour GB, Hillman JL, Yu JY, Tuason O, Daugherty SC, Dam TC, Liu TF, Nguyen DA, Peralta CH, David MH, Lewis SA, Chen AJ, Flores V, Marwaha R, Lo A, Lan RY, Urashl
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                    139
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                                                      TCCGGCCCCAGAGGTGGCCCACGTCTGGGGGGTCACTGCGGCAGCCAAGGCCTGGGGG
                                                                                         Conservative
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                                                                                                                                               Pred.
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                                                                                                                              Mismatches
                                                                                                                                                                                                   708 G; 441 T; 0 U; 0 Other;
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No. 4.
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O, Yap PE, Amshey SR;
DA, Kleefeld Y, Gersti
AJ, Panzer SR, Harris
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osteoporosis
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                                                                                                         Matches
                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                   The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06702-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence of the invention.
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                              New polynucleotides and polypeptides are useful developing a diagnostic marker or medicines for expression and activity, or as a target of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM01893
                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 578; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-723558/69.
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                                                                                                                                                            451 A; 875 C;
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Hio Y, Otsuka K, I
Otsuka M, Nagahari
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Nagahari K, Masuho Y;
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            The invention relates to 625 polynucleotides which have been derived from CC a variety of human tissue sources and which encode novel secreted CC proteins, their complements and sequences that hybridise to them. Also CC included are a vector comprising the polynucleotide, a host cell CC transformed with the vector, the proteins encoded by the polynucleotides, antibodies that bind to the proteins and identification of modulators of CC antibodies that bind to the proteins and identification of modulators of the proteins or the expression of the polynucleotide. The polynucleotides CC can be used as probes for the identification and isolation of full length CC cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The protein is useful in the treatment of CC various immune deficiencies and disorders such as viral infections, actorial infections, fungal infections, autoimmune disorders (e.g. theumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and CC disbetes) and allergic reactions and conditions (e.g. asthma). They are CC disbetes) and allergic reactions and conditions (e.g. Alzheimer's CC disbetes) and allergic reactions and conditions (e.g. Alzheimer's CC disbetes) and allergic reactions and conditions (e.g. Alzheimer's CC disbetes) and allergic partial infections. They are also useful for tissue regeneration, for wound healing CC and in the treatment of burns, inclisions and ulcers. The proteins are CC lymphoid cell deficiencies. The present sequence is one of the 625 cDNA centeriors are conditions as secreted martein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wong GG,
Gulukota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis; disbetes; allergy; astima; neurodegenerative disease; Crohn's disease; hlzheimer's disease; parkinson's disease; liver fibrosis; tumour; coagulation disorder; haemophilia; inflammatory disorder; ulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-2000; 2000US-0194941P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue regeneration; wound healing; haematopoiesis;
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a secreted protein
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2000US-0219467P.
2000US-0215135P.
2000US-0215647P.
2000US-02174880P.
2000US-0217496P.
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2000US-022513P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder su as cancer or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ
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2000US-0251986P
2000US-0251866P
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22-AUG-2000;
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01-SEP-2000;
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14-SEP-2000;
16-NOV-2000;
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2000US-0226668P.
2000US-0227099P.
2000US-022934SP.
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2000US-023943SP.
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### Standard; DNA; 1957 BP.  101 (first entry)  101 (first entry)  1020-001 (first entry)  1020-001 (productive system related antigen DNA SEQ ID NO: 10141.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; gene therapy; ds.  1020-002 (productive system related antigen; reproductive system disorder; gene therapy; gene th
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2000US-0232081P. 2000US-023196RP. 2000US-0232398P. 2000US-0232398P. 2000US-0232401P. 2000US-0232401P. 2000US-0233064P. 2000US-0233064P. 2000US-0234274P. 2000US-0234274P. 2000US-0235834P. 2000US-0236802P. 2000US-0236802P. 2000US-024617P. 2000US-024677P. 2000US-024675P. 2000US-0249211P. 2000US-024921P. 2000US-024929P. 2000US-024929P. 2000US-024929P. 2000US-024929P.

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RESULT 9
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        antiarteriosclerotic; immunosuppressive; antiaheumatic; antiarthritic; antiinflammatory; antiallergic; antiasthmatic; dermatological; nephrotopic; virucide; fungicide; antibacterial; antiparasitic; gene therapy; ds; connective tissues disorder; rheumatoid arthritis; systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; cardiovascular disease; atherosclerosis; myocarditis; cardiopulmonary bypass complication; autoimmune disease; multiple sclerosis; allergic reaction; asthma; rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis; gastrointestinal disease; inflammatory bowel disease; nephritis; gastrointestinal disease;
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used in p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences commber of human reproductive system related antigens. These can be in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encountered to the invention
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 transplant rejection; immune
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69; Conservative
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No. 8
 system disorder;
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   Bruton's disease;
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be used
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14-AUG-2000

14-AUG-2000

18-AUG-2000

22-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

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06-SEP-2000

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14-SEP-2000

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11-JUL-2000
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16-MAR-2000
17-MAR-2000
18-APR-2000
19-MAY-2000
07-UUN-2000
28-UUN-2000
07-UUL-2000
07-UUL-2000
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14-AUG-2000;
14-AUG-2000;
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B-cell lymphoproliferative disorder; HIV; AIDS; inf
chromosome identification; chromosome mapping;
connective tissue related polynucleotide; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-2002;
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2000US-0184664P.
2000US-0198974P.
2000US-0199173P.
2000US-0199173P.
2000US-0215135P.
2000US-0215135P.
2000US-0215135P.
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2000US-0215135P.
2000US-0215135P.
2000US-0215135P.
2000US-0215135P.
2000US-021748P.
2000US-0229345P.
2000US-02252114P.
2000US-02252114P.
2000US-02252114P.
2000US-02252114P.
2000US-02252114P.
2000US-0225266P.
2000US-022575P.
2000US-023575P.
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2000US-02331141P.
2000US-02331141
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27-SEP-2000; 27-SEP-2000;

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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11-DEC-2000;
05-JAN-2001;
17-JAN-2001;
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neoplasias.
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                                                                                                                                                                                                                                                                                                FR-008 polyketide gene cluster,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ADZ51725 standard; DNA; 138203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB;
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nilarity 56.6%;
Conservative
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2001US-0259678P.
2001US-00764847.
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/*tag= b
/product= "ADC lyase, E
complement(3150. .3818)
                                                                   /product= "FAD-dependent
complement(2264. .3037)
                                                                                                                                    Location/Qualifiers complement (574. .1950)
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29-SEP-2000
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      YS,
                  KOREA ADV INST SCI & TECHNOLOGY.
UNIV SHANGHAI JIAOTONG.
      Deng
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/product=
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/product= "Glycosyltransferase,
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complement(10298. .13315)
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                                                                                                                                  omplement (107496.
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omplement(28983. .60860)
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     Jeong KJ,
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Query Match Best Local S Matches

Similarity

55.0%;

Score 36.2; D Pred. No. 53; 0; Mismatches

DB

14; 58;

Length

138203;

0;

Gaps

0

Conservative

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The present invention relates to a gene cluster (ADZ51725) for the biosynthesis of FR-008 polyketides derived from Streptomyces sp. FR-008. CC FR-008 polyketide, a hetaene macrolide having aglycone containing 4-CC aminoacetophenone, has antifungal activity and also high toxicity against CC fields. The gene cluster comprises the following genes: fscA, fscC, fscB fscF, fscE and fscD, which code for modular polyketide synthase (PKS); CC fscF, fscE and fscD, which code for abC transporter proteins; fscRI, fscRI, fscRII, cdes. FiscRIII and fscRIV genes which code for regulator proteins; fscP which CC codes for cytochrome P450 monooxygenase; fscMI which codes for fscRII hich codes for cytochrome P450 monooxygenase; fscMI which codes for glycosyltransferase; fscMII which codes for GDP-ketosugar caminotransferase; fscMII which codes for GDP-mannose-4,6-dehydratase; fscO which codes for FAD-dependent monooxygenase; pabAB which codes for CC lyase. The genes of the gene cluster of the invention can be used to CC develop recombinant microorganisms capable of producing FR-008 cc polyketides, also to increase the productivity of the existing FR-008 cc modification.
  Sequence 138203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1; 22pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New gene cluster for the biosynthesis increasing the productivity of FR-008 008 polyketide variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WRI, 2005-322033/33.
P-FSDB; ADZ51726, ADZ51727, ADZ51728, ADZ51729, ADZ51730, ADZ51731,
ADZ51732, ADZ51733, ADZ51734, ADZ51735, ADZ51736, ADZ51737, ADZ51738,
ADZ51739, ADZ51739, ADZ51740, ADZ51741, ADZ51742, ADZ51743, ADZ51744, ADZ51745,
                                             modification.
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BP; 18153 A; 48202
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polyketides
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  16506 T;
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es or to produce new
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CCCGGCGAC 109259
                                                          GETCAGGGCCGCCGGGCCGGGACGCCGCCGGGGAGGGCGCCGGTCCCGGTCACCGGGTTC 109250
                                                                                       CGTCAGGTGGGTGACGGCAGGGGTCTTGCCATGGTGGGCACAGGGGGCTGCATACAGCTTA 161
                                                                                                                       GGTGAGGCACCACAGCGGGGGGTCGGTGCGGGCGTCGCCGAGCGCCTGGACCAGGGTCGC
                                                                                                                                                   GGTGACTCACCCCCATGTGGCTGGAGGTGAGGGAGCCTCCTGAGGCAGGGCCAGGGCAGC
                           CTCAGTGAC
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RESULT 11
ADQ56739
ID ADQ56
XX
AC ADQ56
XX
AC ADQ56
XX
AC ADQ56
XX
Canir
CW Canir
KW Canir
KW Canir
KW toxvi
KW toxvi
KW toxvi
CM protic
XX
XX
VX
VX
Z3
PN WO200
XX
PD 29-JI
                                                                                                                              Novel canine microarray-related DNA sequence SeqID8041
                                                                                                                                                                                              ADQ56739
                                                                                                                                                                                              standard; DNA; 546
                                                                                                                                                     (first entry)
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canine microarray; drug screening; toxicity assay; environmental pollutant; cellular response; gene expression profile; toxic response; liver necrosis; fatty liver disease; WO2004063324-A2 Canis familiaris toxic response; liver necr
protein adduct formation;

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RESULT 12
AAQ94044/c
ID AAQ940
XX
AC AAQ940
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AC AAQ940
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                                                                                                                                                                                                                                                                                                                                                                                                                   문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cc sequences and the construction of canine microarrays containing a carificant portion of the canine genome. The isolated canine nucleic acid sequences of the invention may be useful for drug screening and consicity assays. The invention is therefore useful for assessing the climatet including toxicity, of a compound, pharmaceutical agent or convironmental pollutant on a cell or living organism. The methods are useful for detecting genes that are up- or down-regulated in canines in a disease state. The sequences are useful as diagnostic agents or markers condulate gene expression or activity. The database is useful for gene expression profile. It is also useful as a target for agents that compound producing electronic Northerns that allow the user to determine the cell type or tissue in which a given gene is expressed and to allow continuity of a toxic response to one or more individual compounds. The methods are useful for determining the congration are useful for predicting at least one toxic response or the confidence of the liver necrosis, fatty liver contains and those of the liver necrosis, fatty liver pathologies such as those of the liver necrosis, fatty liver heart, brain or testes, or other pathologies associated with at least one of the toxins. The methods are also useful for predicting or elucidating the potential cellular pathways influenced, induced or modulated by the compound or test agent due to the similarity of the expression profile compound or test agent due to the similarity of the expression profile compound or heaving the similarity of the expression profile compound or test agent due to the similarity of the expression profile compound or heaving the similarity of the expression profile compound or test agent due to the similarity of the expression profile compound or test agent due to the similarity of the expression profile compounds. The methods are also useful for use during the constitution of a canine blacroarray of the similarity of the expression profile considered in the profi
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Best Local
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     16-NOV-1995
                                                  AAQ94044;
                                                                                                AAQ94044 standard; DNA; 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 546 BP; 96 A; 148 C; 161 G; 130 T; 0 U; 11 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid molecule, useful for drug screening and toxicity assays or for assessing the impact, including toxicity, compound, pharmaceutical agent or environmental pollutant on a ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production of a canine microarray of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention is related to a novel isolated canine nucleic sequences and the construction of canine microarrays contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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PFIZER PROD INC
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                                                                                                                                                                                                                          NNNGCTGCTATCTTTGAGACAGA
                                                                                                                                                                                                                                                                     ACCAGGTCTGAGTCAGAGCCAGA 462
                                                                                                                                                                                                                                                                                                                                                         CCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGGGGCTGGGCTGGGCAGGCC 439
                                                                                                                                                                                                                                                                                                                     CCCACCCTGGCGNNGCCACAGCAGCCCNTCACGGCAANNAACCCNTGCAGCCTGGGGNCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 8041; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.4%;
50.3%;
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Pred. No. 13;
0; Mismatches
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                                                                                                                                                                                                                                                           The putative ALD gene identified in the distal part (had deletions in 1 or several exons in 6 of 85 indeports examined. The gene has 10 exons and 9 introns, shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                               Sequence 704 BP; 127 A; 235 C; 205 G; 135 T;
                                                                                                                                                                                                                                                                                                                              Claim 3; Fig 7B; 39pp; English
                                                                                                                                                                                                                                                                                                                                                             New nucleic acid responsible for adreno-leuco-dystrophy - related probes, proteins and antibodies, useful for diagnosis and treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-215721/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mandel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA2108606-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-OCT-1993;
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                                610
506 CAGTCCTCCTGGCCACCTGAGAACAGCCTGTAGAGAGGC 544
                                                               446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy;
                                                                                                                                                                 82;
                                                                                                                                                                                 Similarity
                                                                                                                          CTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGGGGCTGGGGCTGGGCAAGGCCACCAGG
                              TCAGCACCTGCAGCAGCAGCAGGGGGGGGGGTCACTCATAGGGAGCGGACAGCCTTACCTC
                                                               TCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCCAGCACTGCCCGCCGCCGCCTCTGCGATG
                                                                                              CAGAAGCACATGGAGGTCCCTGAGTGAGGGAGCGGGGATAGGAGGAGCTGGGGCAGCAGG
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                                                                                                                                                               Conservative
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/note= "150 base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "base n at position 1 represents the of intron-2, not given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= d
/label= Exon-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag=
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'note= "150 bases of
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                                                                                                                                                                               Score 35.8;
Pred. No. 16;
                                                                                                                                                               Mismatches
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                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                          part of chromosome independent ALD pat
                                                                                                                                                                                                                               U; 2 Other;
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RESULT 14
ABV51994/c
ID ABV519
XX
AC ABV519
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AC ABV519
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ABQ90455/c
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Best Local :
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                                               ABV51994 standard;
                                                                                                                                                                                                                                                       Sequence 1263
                                                                                                                                                                                                                                                                                       The invention relates to a novel DNA array giving a representation of a number of Methylococcus capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of M. capsulatus, and for studying gene expression on a genemic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birkeland NK,
Lillehaug JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M. capsulatus gene #440 for DNA array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABQ90455;
 17-SEP-2002
                          ABV51994;
                                                                                                                                                                                                                                                                                                                                                                                                            Methylococcus capsulatus genes, oligonucleotides representative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-JAN-2001; 2001NO-00000235.
12-JAN-2001; 2001NO-00000239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JAN-2002; 2002WO-NO000019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200255655-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methylococcus capsulatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Micro array; gene; ds; differential expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                            Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                  capsulatus genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel DNA array useful for determining differential expression
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                                                                                                                               485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIFOB
                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SL;
                                                                                                                                  CTGCCCGCCCCCTCTGCGATGCAGTCCTCCTGGCCACCTGAGA 527
                                                                                                                                                                                GGGCTGGGCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCCAGCA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGATCTTCAGGGGGCCCTCCACACGGACACCAGACCGGC
                                                                                                          CTTTTCGCCGCCGCGGCGCGACGACCTCCGAGACGCCCAGGA 335
                                                                                                                                                           GGGATGGGCAGGCGCCTGGCCGGCCCGAGATAGGCATAGAGCGGCAGCCCCGCA
                                                                                                                                                                                                                                                                                                                                                                           Page 257-258; 678pp; English
                                                                                                                                                                                                        Conservative
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                       BP; 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STIFTELSEN UNIV BERGEN
                                                CDNA; 568
                                                                                                                                                                                                                  59.2%;
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                                                                                                                                                                                                                                                      A; 385 C;
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                                                ВP
                                                                                                                                                                                                                   Score 35.8;
Pred. No. 19
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                                                                                                                                                                                                                                                                                                                                                                                                               comprises polynucleotides or for a selective number of Methylococcus
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Durkin A
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Best Local Similarity
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a thorapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer has metastatized in a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (ii) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                            Sequence 568 BP; 110 A; 169 C; 154 G; 135 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, use for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-2001; 2001WO-US005171
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                              G-CACTGCCGCCGCCTCTGCGATGC 506
                                                                                             GCTGGGCTGGGCAAGGCCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCCA 481
                                                                                                                              CGAGGTAGGCAGAGAAGGGCAAGTGAGAGGGCGAAGGCCCAGGGATGGCGGGTGGGGGGG
                                                                                                                                                             CAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGGG
                                                                                                                                                                                             CCGGGGGACACCATGGTCCTCACCCAGGTTACTTGTCCATGCCCTTCCCACTGGAGAGGA
                                                                                                                                                                                                                            CAGGGTCCCATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCTCGCAGTCATGAAAC
                                                              CCTGAGCATTGGGCCTTCCCCTTTCTCTCCCCAGACCCCTGGACATGCCCTTGGCGGCAA
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2000US-0211314P.
2000US-0219007P.
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Pred. No. 17;
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AAS19511

standard;

DNA; 1785

ВP

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Query Match
Best Local 9
                                                                                                            Matches
                                                                                                                                                                                                       The present invention relates to novel single nucleotide polymorphisms (SNPB) in the human myeloproliferative leukaemia virus oncogene (MPL) gene located on chromosome 1p34, and methods for haplotyping and/or genotyping the MPL gene. The methods of the invention make use of allelespecific oligonucleotides (ASOs) as probes and primers and/or primer-extension oligonucleotides for detecting MPL gene polymorphisms. The polymucleotides and scoppounds are useful for the treatment of diseases associated with MPL activity, such as congenital amegakaryocytic thromobocytopaenia (CAMT). The present sequence represents a reference sequence for human MPL gene exons 9-10. Note: This sequence encodes for
                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide polymorphisms in the human myeloproliferative leukemia virus oncogene (MPL) gene, useful for studying the function of and expressing MPL protein for use in screening drugs for treating diseases related to MPL activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chew A,
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                                                                                                                                                                    Sequence 1785 BP;
                                                                                                                                                                                                                                                                                                                                                                   Claim 27; Fig 3; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-APR-2000; 2000US-0197839P
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57; Conserv
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                      TGA CGGCAGGGTCTTGCCATGGTGGGCACAGG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Choi JY, Koshy B,
                                                      CCCATGTGGCTGGAGGTGAGGGAGCCTCCTGAGGCAGGGCAGGCCAGCCGTCAGGTGGG 112
TGAGGGCGGGCTCCGGCCCGGGTGGGCCGAAG
                                                                                                           6.3%;
llarity 61.3%;
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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BE502665 hz20e10.x
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#### ALIGNMENTS

ORIGIN	FEATURES BOUICE	COMMENT	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	RESULT 1 AG133394 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM
/organism="Pan troglodytes" /mol type="genomic DNA" /db_xref="taxon:9598" /clone="FyB-146A21.R" /sex="male" /cell_type="lymphoblast" /clone_lib="PTB Chimpanzee Male BAC Library"	clone tracking errors.  PRIMERS Sequencing: M13Rev LIBRARY Vector : pKS145 R.Site 1 : SacI R.Site 2 : SacI Location/Qualifiers 1 . 603	and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of	(Dases 1 to 603)  2 (Dases 1 to 603)  7 (Dases 1 to 603)  8 (Dases 1 to 603)  Totoki, Y., Watanabe, H. and Sakaki, Y.  10 (Direct Submission  10 (Direct Submission)  11 (Direct Submission)  12 (Direct Submission)  13 (Direct Submission)  14 (Direct Submission)  15 (Direct Submission)	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Pan.  1  Pujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB	AG133394 Fan troglodytes DNA, clone: PTB-146A21.R, genomic survey sequence. AG133394 AG133394.1 GI:16663072 GSS. Pan troglodytes (chimpanzee) Pan troglodytes (chimpanzee) Pan troglodytes

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                                                                     83;
                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.linl.gov/bbrp/inage/inage.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 614 Std Erro
Seg primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.
1 (bases 1 to 312)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tw62all.x1 NCI_CGAP_Ut3
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CCGCCCATGCTGGCTCAGTTCCTGCCCCCTGGAGGGAAGGGGGCCCGAGGGGGCTTCCCGTCCC
                                 CCCCCAACGTTGCACACTCACTGCCTTTGCAGGGTTGGGGCTTCCAGTCACAGGGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGTCTTGC 602
                                                                  7.3%;
nilarity 54.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 303.
Location/Qualifiers
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                                                                                                                                                        /clone_lib="NCI_CGAP_Ut3"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"
                                                                                                                                                                                                                                              /tissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                   clone="IMAGE: 2264252"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.8%;
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                                                                  Score 41; DB Pred. No. 8.4; 0; Mismatches
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Pred. No. 7.7e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw 8p, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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AL053013
SAGSVVSSASSSSSSSSSSSVSCSSVASSMSCSSBSSSSASSSSSSSSSSASCASCSCCCT
                                            GGGCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCCAGCACTGCC
                                                                                         CATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCTCGCAGTCATGAAACCAAGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
|mol_type="genomic_DNA"
|/db_xref="taxon:7227"
|/clone="BACR19D16"
|/clone lib="RPCI-98"
|/note="end : TET3"
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Pred. No. 15;
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Neopteara; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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                                                                                                    ATGAAACCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGA 414
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
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                                                                                                                                                                                                                                                                                                                 Score 40; DB 1
Pred. No. 19;
11; Mismatches
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AGENCOURT_8803539 NIH_MGC_101 Homo
5', mRNA sequence.
B0948345
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High quality sequence start: 24
High quality sequence stop: 233.
Location/Qualifiers
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, w
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Mammalia; Eutheria;
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Contact: Robert Strausberg, Ph.D.
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Similarity 51.7%;
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                                                           AGTGAGCAAGAGGCACTTGTTCTCCTTGATGGCACCCAAGCAGCCCACGAAGCC 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="epidermoid carcinoma, cell line"
/lab host="DHIOB (phage-resistant)"
/clone libs="NIH_MGC_101"
/clone libs="
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/db_xref="taxon:9606"
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Pred. No. 24;
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Best Local Similarity
Matches 43; Conserv
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
               AI289637 321 bp mF
qw29d03.x1 NCI_CGAP_Ut4 Homo sapiens
mRNA sequence.
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit
mRNA sequence.
AI289637
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Submitted (23-JUL-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (B-mail:
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Drosophila melanogaster
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/mol type="genomic DNA"
/db xref="taxon:7227"
/clone="BACN37L08"
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/plasmid="pBeloBAC11"
/note="end : SP6"
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14.0%; Pred. No. 25;
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Mammalia; Eutheria;
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1 (bases 1 to 321)
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                               Ehrhartoideae;
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            chartoideae; Oryzeae; (bases 1 to 637)
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 Stum, D.,
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   Yost, D.,
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OB_Ba0066B18.f OB_Ba Oryza brachyantha genomic clone OB_Ba0066B18 5', genomic survey sequence.
CL542202
CL542202.1 GI:47612804
Oryza brachyantha
Oryza brachyantha
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 2780 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 290.
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Contact: Robert Strausberg, Ph.D.
Email: cgspbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone lib="NCI CGAP Ut4"
/clone lib="NCI CGAP Ut4"
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/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.48 kb. Life Technologies catalog #
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/clone="IMAGE:1992485"
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Pred. No. 32;
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           Streptophyta; Embryophyta; Tracheophyta; yta; Liliopsida; Poales; Poaceae;
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Rao, K.,

Luo, M., Jetty, R.,

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AUTHORS
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University of Arizona
Forbes Building Room 303, Tu
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                  1 (bases 1 to 867)
NIH-MCC http://mcc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                        CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
Plate: LLCM2609 row: h column: 11
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BQ931784
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Contact: Rod A. Wing
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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AGENCOURT 8803536 NIH MGC 101
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Seg primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
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BACKWARD: CAC TCA TTA GGC CCCA
INSERT Length: 145000 Std Error
Plate: 0066 row: B column: 18
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                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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Location/Qualifiers
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/lab_host="PH10B"
/clone_lib="OB_Ba"
/clone_lib="OB_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2:
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Pred. No. 53;
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sapiens cDNA clone
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Query Match
Best Local Similarity
                                                                                                              Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sec

Clone distribution: NCI-CGAP clone distribution in/
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 488 Std Error: 0.00

Geor primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A1970105 393 bp mRNA linear EST 20-OCT wq89c02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IWAGE:2479202
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria;
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/db xrefe="navon:9606"

/db xrefe="navon:9606"

/clone="IMAGE:6426298"

/tissue_type="epidermoid carcinoma, cell line"

/clone="ibb="NIH_MGC 101"

/clone_lib="NIH_MGC 1
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/organism="Homo sapiens"
/mol_type="mRNA"
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Pred. No. 57;
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RESULT 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LinL at: hmage.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 419.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.

1 (bases 1 to 481)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy
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EST.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/note="Vector: pT773D-Pac (Pharmacia) with a modified note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplied cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
/note=TOrgan: pancreas; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #:
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/lab_host="DH10B"
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                                                                                                                                                                                     /organism="Homo sapiens'
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                 /lab_host="DH10B"
/clone_lib="NCI_C
                                                                                                                                 tissue_type="adenocarcinoma"
                                                                                                                                                               /clone="IMAGE:2877161"
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Pred. No. 55;
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SOURCE

KEYWORDS

ACCESSION

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TITLE
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Best Local
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                                                                                                                                     Matches
                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consorthum/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1852 Std Error: 0.00
seg primer: -40UP from Gibco
                                                                                                                                     69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hominidae; Homo.

1 (bases 1 to 523)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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EST.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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Similarity 56.6%;
                                                                                                  CCCCCAACGTTGCACACTCACTGCCTTTGCAGGGTTGGGGCTTCCAGTCACAGGGTCCC
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                               ATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAACCAAGGGAGG
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Location/Qualifiers
                                                                                                                                     Conservative
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                                                                                                                                                                                                                     /clone lib="NCI_CGAP_Pan1"
/note="Torgan: pancreas; Vector: pCMV-SPORT6; Site_1: Stote_2: NotI; Cloned unidirectionally. Primer: Oligo (Average insert size 1.72 kb. Life Technologies catalog 11548-013"
                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                           clone="IMAGE:2419743"
                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                         tissue_type="adenocarcinoma"
                                                                                                                                                   6.7%;
56.6%;
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Pred. No. 6
                                                                                                                                                     Score 37.8;
Pred. No. 65;
                                                                                                                                       Mismatches
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ACCESSION
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SOURCE
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AUTHORS
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ACCESSION
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CF795053/c
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Best Local Similarity
Matches 91; Conserv
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Sus scrofa (pig)
Sus scrofa
                              AW975697.1
EST.
                                                                                           AW975697 554 bp mRJ
EST387806 MAGE resequences, MAGN Homo
AW975697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: TMW8015 row: K column: 23
Seq primer: TAGAAGGCACAGTCGAGG.
Location/Qualifiers
1. .592
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Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Nonneman, D.J., Wray, J.B. and Keele, J.W.
Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
Unpublished (2003)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   592
CF795053
891143 MARC 4PIG Sus scrofa
CF795053
CF795053.1 GI:37799626
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 402 762 4366
Fax: 402 762 4390
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAGGAAACCAGGGAAGACTGGATATAAAATACCGAGGGGGGGCTTGTTTGAGTATGTCA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCATGAAACCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGA 412
                                                                                                                                                                                                                                                                                                                               CCGTCCAGGGCTCGGCGTTCGCCCTCTTCACCTTCTGCGTCCTGTGCACCAGGGCTCAGC
                                                                                                                                                                                                                                                                                                                                                                                         TGGTCCCCAGCACTGCCCGCCGCCTCTGCGATGCAGTCCTCCTGGCCACCTGAGAACAGC 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGCGGCCAACTACCTCGGGGAGGTCGTCGAGTGGGTGCGGCTACGCCCTGGCCAGCTGGT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGGGTGGGGCTGGGCCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGC 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="MARC 4PIG"
/clone lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
/note="Vector: pcDNA3.1; Site 2: NotI;
/n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Sus scrofa"
                                                                GI:8166915
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Pred. No. 76;
0; Mismatches 89; Indels
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ofa cDNA 3', mRM
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ens cDNA,
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REFERENCE
AUTHORS
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AA983291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        425 TTCCTGA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485 AGAAGGGGCTGAAGAAAGGGCAGCTGTCTTGGGGTACACTGGGAACTGGAAGGAGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assessment of gene expression patterns in a model metastasis using a 19,200 element cDNA microarray Unpublished (2000) Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                oq56e01.sl NCI_CGAP_Kid5
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Hegde, P., Qi, R., Aberna
Holt, I.E., Saeed, A.I.,
                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                          Hominidae; Homo.
1 (bases 1 to 294)
                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
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Plate: 352
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nilarity 55.9%;
Conservative
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                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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Pred. No. 84;
O; Mismatches
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IMAGE:1590360 3',
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Search completed: March 25, 2006, 18:16:22 Job time : 3245 secs
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Best Local Similarity
Matches 69; Conserv
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                                                                  371 CT 372
                                                                                                          311 ATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAACCAAGGGAGG 370
                                                                                                                                  159 CCGCCCATGCTGGCTCAGTTCCTGCCCCTGGAGGGGAAGGGGCCGAGGGGCTTCCCGTCCC 218
                                                                                                                                              251 CCCCCAACGTTGCACACTCACTGCCTTTGCAGGGTTGGGGGCTTCCAGTCACAGGGTCCC 310
                                                                                        Insert Length: 890 Std Error: 0.00
Seg primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 273.
Location/Qualifiers
1. .294
                                           CT 280
                                                                                                                                                                        6.6%; Score 37.2; DB 1; Length 294; ilarity 56.6%; Pred. No. 84; Conservative 0; Mismatches 53; Indels
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Minimum
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
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9: /cgn2_6/ptodata/1,
9: /cgn2_6/ptodata/1,
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Gapop 10.0 , Gapext 1.0
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      Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
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US-09-902-540-604
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Sequence 15732, A
Sequence 11007, A
Sequence 18033, A
Sequence 604, App
Sequence 12065, A
Sequence 11090, A
Sequence 11, Appl
Sequence 11499, A
Sequence 11499, A
Sequence 15483, A
Sequence 15980, A
Sequence 15980, A
Sequence 1958, A
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Sequence 15436, A
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	10196, Ā	6132, Ap	194766,	91825, A	15962, A	12068, A	13690, A	16322, A		9690, Ap	9561, Ap	9606, Ap	-	20, Appl	20, Appl	15472, A	18, Appl	17, Appl	16967, A	747, App	14580, A

#### ALIGNMENTS

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Best Local S
Matches 103
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Patent No. 6812339
GENERAL INFORMATION:
                                                                                              17528
                                                             17588 CCACCGGAGCCCCACCCTGCGTGGTCCCCACCCGGAGCATCGCTTGGGCCCCCGGCACTCAC
259 CGTTGCACACTCACTGCCTTTGCAGGGTTGG
                                                                              139 GCACAGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCCCTGGTGCCAGCCTCTGGA 198
                                                                                                                                 6.8%; Score 38.2; DB 3; Length 23856; al Similarity 48.8%; Pred. No. 1.4; 103; Conservative 0; Mismatches 108; Indels 0;
                          AGTGAGCAGGAGGCACTTGTTCTCCTTGATGGCACCCAGGCAGCCCACGAAGCCGATGGC 17469
                                         0;
                                                                                                                                  Gaps
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CATGACAAAGGCGCCGGTGATGATGAGCAGG 17438

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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
ITILE OF INVENTION. EST's and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 18033
LENGTH: 474
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-949-016-14107; Sequence 14107, Application US/09949016; Patent No. 6812339
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US-09-621-976-18033
; Sequence 18033, Application US/09621976
; Patent No. 6639063
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FRANCEQ for Windows Version 4.0
SEQ ID NO 14107
LENGTH: 19319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 69; Conserv
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                                                    Query Match
                                                                                   -09-621-976-18033
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                           FEATURE: misc_feature
                                                                                               LOCATION: 16
OTHER INFORMATION: n=a, g, c
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          Local Si.
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                                  Similarity
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                 6.5%; Score 36.6; DB 3; llarity 13.7%; Pred. No. 1.1; Conservative 148; Mismatches 173;
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llarity 56.6%;
Conservative
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                                               Length 474;
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                                              RESULT 5
US-09-902-540-604
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Sequence 604, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION:
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APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 6966
LENGTH: 954
TYPE: DNA
TYPE: DNA
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Myxococcus xanthus US-09-902-540-6966
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US-09-902-540-6966/c
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                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                               Match 6.2%;
Local Similarity 53.7%;
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344
                                           527 AACAGCCTGTAGAGAG 542
                                                                                              404
                                                                                                                                                                                                                           407 TAGTGAGAGGGTGGGGCTGGGCAAGGCCACGAGTCTGAGTCAGAGCCAGAGGCA 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 WAAAARGGWTWA 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97
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                                                                                                                          GGAAGCTGGTCCCCAGCACTGCCCGCCGCCTCTGCGATGCAGTCCTCCTGGCCACCTGAG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WYYTTYYKRMCCYYMRKTTYCMMMWYSRWWRGSMWTARGAWWMCYWWYYYMAARKKKXMW
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                                                                                              CGGCTCCCCTTGACGGGAATCCATACCCGGACGGCCATGCAGTCCCCCTGGGCTTCTTCG
                                                                                                                                                                                            TCGTGCGCGTGCCGCTTCGAGGAGCCCCACGAGCACGTCCTTGGCCGCGTCCGTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYMMCYYYYMMYKGGRMYWWWRGGMWKRMYWMYKKKSMWKGSCMWKRAWWARKTTYYTWA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTTACTCAGTGACAATCGAGTCCCTGGTGCCAGCCTCTGGAAGTCTGGAAGTGAGCAAT 216
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AGCTGCCAGTAGCGAG
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                                                                                                                                                                                                                                                                                           Conservative
329
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Pred. No. 3.4;
0; Mismatches
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 604
LENGTH: 4050
TYOD: NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12065, Appl. Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000.04-14
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: (1)...(4050)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                       ENGTH: 108440
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                                                                                                                                                      Local Similarity
                                                             81526
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126 CTTGCCATGGTGGGCACAGGGGCTGCATACAGCTTACTCAGTGA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         527
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                                                           AGGTGGTGAAACCACTATGGGCCTGGCCAAATCAGCAAGAAGGGGGCTGGAGGAAGGGCA 81585
                                                                                             GGAAGCTGGTCCCCAGCACTGCCCGCCGCCTCTGCGATGCAGTCCTCCTGGCCACCTGAG 526
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                                                                                                                                  Score 35.2; DI
Pred. No. 16;
0; Mismatches
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Pred. No. 5
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                                                 Query Match
Best Local S
Matches 92
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 14090
                                                                                                                                                                                                                                                                                                           SEQ ID NO 11
                                                                                                                                                     IENGTH: 1338
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (513)
OTHER INFORMATION: unsure
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: COSMAN, DAVÍD J.
TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES
FILE REFERENCE: 2990-A
                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/843,905A
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/200,198
                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-04-28 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bird, Timothy APPLICANT: Cosman, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 108441
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      364 AGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGGGGC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 CTTGCCATGGTGGGCACAGGGGCTGCATACAGCTTACTCAGTGA 169
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                                              6.2%;
1 Similarity 49.2%;
92; Conservative
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58.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 35.2; DI
; Pred. No. 16;
0; Mismatches
                                              Score 35; DB 3; Length 1338; Pred. No. 4.4; 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 108441;
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794 AGGACGGCTCTCTCATCGACCTGTGTGGGGCCACACTGCTGTGGCGCACACCGGCGGGGC

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RESULT 10

US-09-099-016-14499/c

; Sequence 14499, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
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US-09-949-016-13882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 13882
LENGTH: 42610
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13882, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.2%;
Best Local Similarity 46.8%;
Matches 110; Conservative
                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-4-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAACCAAGGGAGGCT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTGCCCGCCGCCTCTGCGATGCAGTCCTCCTGGCCACCTGAGAACAGCCTGTAGAGAGG 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGGCAGGGTGGGGTGAGGCCCCAAGGAAACCATGTGGACTGAAGGGGAAGGGAAGAGGGCAG
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Pred. No. 14;
0; Mismatches 125; Indels
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OF DETECTION AND USES THEREOF
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RESULT 12
US-09-949-016-15483/c
· sequence 15483, Application US/09949016
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TYPE: DNA
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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTMARE: FastSEQ for Windows Version 4.
; SEQ ID NO 14499
; LENGTH: 11276
                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens 
US-09-621-976-17564
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                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 17564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17564, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              Query Match 6.0%;
Best Local Similarity 51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
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LOCATION: (1)...(11276)
OTHER INFORMATION: n = A,T,C
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ORGANISM: Human
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Local Similarity 51.3%;
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                                                                                                                                                                      166 AGGAAGTTGTCGCCGCGGCCATTTCCCCCCAGTGCCGCAACTTGCTGGCCTTGGAGGGGGA 225
                                                                                                                                                                                               CGCAGTCATGAAACCAAGGGAGGCTTGGG 376
                                                                                 GGAGCGCCGAGGCAGTGACTGCGACGCAAACATCAAACCAGATGCAAACAGATTCATTAT
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CTCCATCCCCTAATCCTGTGTCACCTGTG
                                                                                                                       GGGGCTTCCAGTCACAGGGTCCCATCCACGTACCAGGCCAGGTGGCTGCAGAAGGTCCCT 347
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Pred. No. 6.6;
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US-09-949-016-15980/c
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, NAME/KEY: misc_feature
; LOCATION: (1)...(6872)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-15483
                                           US-09-949-016-15980
                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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Best Local S
Matches 68
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
                                                                                                                                                                             SOPTWARE: FastSEQ for Windows Version SEQ ID NO 15980 LENGTH: 239527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15980, Application US/09949016 Patent No. 6812339
    Query Match
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CCURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-09-08
NUMBER: OF SEO.ID NOS: 207012
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SEQ ID NO 15483
LENGTH: 6872
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                                                           OTHER INFORMATION: n = A,T,C
                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(23952
                                                                                                                                     ORGANISM: Human
                                                                                                                                                              TYPE: DNA
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Pred. No. 16;
  Score 33.8;
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Length 239527;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human
FILE REFERENCE: GENSET .054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 364
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                                                               GSGCSWCKSCGGSSYYCRSYSSMGKCSRCTCCMGG
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Mismatches
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Sequence 94858, Application US/09949016
PAtent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION

AND USES THEREOF

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 94858
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-94858
                                                                                                                                                                                                                                                                                                                                 Query Match 6.0%; Score 33.6; DB 3; Length 601; Best Local Similarity 50.6%; Pred. No. 8.4; Matches 78; Conservative 1; Mismatches 75; Indels
269 AGGAACAGCATCTGGAGACCTGACCACCCCTCYT 302
                                                  466 AGGAAGCTGGTCCCCAGCACTGCCCGCCGCCTCT 499
                                                                                                          209 TGAGTAGCAGGGATGGGCTGGGCAGCTGGGGACCCCTGGGGCTCCTCCATGAGACAAGA 268
                                                                                                                                                   406 TTAGTGAGAGGGTGGGGCTGGGCCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGC 465
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음 성 유왕 8 5 Search completed: March 25, 2006, 15:02:01 Job time: 202.5 secs

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Perfect score:
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    EST: +
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4: 995
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Gapop 10.0 , Gapext 1.0
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   9b_est4:
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10 AG133394
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AL053013 Drosophil
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AL108460 Drosophil
A1289637 qw29d03.x
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BQ931784 AGENCOURT
A1970105 wq89c02.x
A781818367 wk59h08.x
CF795053 891143 MA
A2983291 cq56e01.8
BG230743 maf39e01.
BU194839 AGENCOURT
A1651114 wa97h01.x
BE502665 ht20e10.x
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BE502405 hy12f03.x
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6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6		6.6				6.6
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### ALIGNMENTS

O <sub>R</sub>	FF EF	8	RE	RE	SESSEC
ORIGIN	FEATURES BOURCE	COMMENT	JOURNAL REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS	AG133394 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
/organism="Pan troglodytes" /mol_type="genomic DNA" /db xref="taxon:9598" /clone="PTB-146A21.R" /sex="male" /cell_type="lymphoblast" /clone_lib="PTB Chimpanzee Male BAC Library"	Vector : pKS145 Vector : pKS145 R.Site 1 : SacI R.Site 2 : SacI. Location/Qualifiers 1603		Unpublished 2 (bases 1 to 603) Pujlyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.  1  1  Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  BAC end sequences of Library PTB	

Length 603;

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                                                                    83;
                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph. D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 61 Std Error: 0.00
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 312)
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Location/Qualifiers
                                                                  7.3%; llarity 54.2%; Conservative
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                                                                                                                                                   /clone lib="NCI CGAP Ut3"
/note="Corgan: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"
                                                                                                                                                                                                                                                          /tissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                clone="IMAGE:2264252"
                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI disestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                             430
                                                                                                                                                                                      864 SGTSSACVKCNASSSCGCCGCGMABCCMCSSSSSCCGSASARGVKVRASGGAGKRGGGSG
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                                                                                                                                                                                                                                                                                  924 SBSCSCSCSSBSCSSSSMSTSSSNSSBCSSCSSSBSSSSTSSMSSSSBSSSSGSSSSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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GSS.
Drosophila melanogaster (fruit fly)
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope.
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Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fly), genomic survey sequence.
AL053013
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GGGCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCCAGCACTGCC
                                                                                           CTTGGGAAACCACATCTGAAGGGCATGGCTTTG 403
                                                                                                                                         GCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGGGGCTGGGCT 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Drosophila melanogaster"
|mol_type="genomic DNA"
|db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="BACR19D16"
/clone_lib="RPCI-98"
/note="end : TET3"
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13.2%;
                                                                                                                                                                                                                                                                                                                                                                           135;
                                                                                                                                                                                                                                                                                                                                                                                                Score 40.4;
Pred. No. 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                       415
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (fruit fly)
Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope.
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                                                                  STSASGSGSWSAGGGSGSTGSTSSSSSSSSSTSTSSSSVSSGSKSSTBSSGSBSSSGSSSS 733
                                                                                                             ATGAAACCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGA 414
                                                                                                                                                                                                      CCAGTCACAGGGTCCCATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTC
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/organism="Drosophila melanogaster"
/mal_type="genomic DNA"
/mal_type="genomic ZNA"
/db_xref="taxon:7227"
/clone="BACR19D16"
/clone_lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="end : TET3"
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BQ948345
BQ948345.1 GI:22363823
EST.
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High quality sequence start: 24
High quality sequence stop: 233.
Location/Qualifiers
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 915)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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AGENCOURT 8803539 NIH MGC 101 Homo
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http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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Similarity 51.7%;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
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                                                                                                                                    CCACCGGAGCCCCACCCTGCGTGGTCCCACCCGGAGCATCGCTTGGGCCCCGGCACTCAC
                                                                TCCTGAGGCAGGGCCAGGGCAGCCGTCAGGTGACGGCAGGGGTCTTGCCATGGTGG 138
   AGTGAGCAAGAGGCACTTGTTCTCCTTGATGGCACCCAAGCAGCCCACGAAGCC
                                                                                                                                                                                                                                                                         TCCGGCCCCAGAGGTGGTGCCCACGTCTGGGGGGTCACTGCGGCAGCCAAGGCCTGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="spidermoid carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clome_lib="NIH_MGC_101"
/clome_lib="NIH_MGC_101"
/clome_lib="NIH_MGC_101"
/clome_lib="NIH_MGC_Li01"
/clome_lib="NiH_
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Pred. No. 24;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a NRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
               321 qw29d03.x1 NCI_CGAP_Ut4 Homo mRNA sequence.
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
Drosophila melanogaster
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AL108460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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 AI289637
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                                                                                                                                                                                                                                                                                                                                AAACCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGG
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                                                                                                                                 ASASASVS 1069
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                                                                                                                                                                 AGAGAGGC 544
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/clone="BACN37L08"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Drosophila melanogaster"
/mol_type="genomic DNA"
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Pred. No. 25;
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                              bp mR
sapiens
                                                 mRNA
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                                RNA linear EST 21-DEC-1998 CDNA clone IMAGE:1992485 3',
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                  GSS.
Oryza brachyantha
Oryza brachyantha
Oryza brachyantha
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70;
                                                                                                                                                                             CL542202 637 bp DNA linear GS:
OB Ba0066B18.f OB Ba Oryza brachyantha genomic clone
OB Ba0066B18 5', Genomic survey sequence.
CL542202
CL542202 GI:47612804
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2780 Std Error: 0.00
Kim, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 2780 Std Error:
Seq primer: -40UP from Gibco
High quality sequence stop: 290.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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EST.
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Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria;
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                                              Ehrhartoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CT 372
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                                                                                                                                                                                                                                                                                                                                                                                      CT 292
                  rhartoideae; Oryzeae; (bases 1 to 637)
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  Yu, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Ut4"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="serous papillary carcinoma, high grade,
pooled tumors"
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/db_xref="taxon:9606"
/clone="IMAGE:1992485"
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  Stum, D.,
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Pred. No. 32;
    Yost, D.,
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    Rao, K., Luo, M., Jetty, R.,
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Matches 58
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Bource
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                                         cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
http://image.llnl.gov
http://image.llnl.gov
                                                                                                                                                           1 (bases 1 to 867)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                             5', mRNA sequence.
BQ931784
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BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 145000 Std Error: 0.00
Plate: 0066 row: B column: 18
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
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Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson,
Tel: 520 626 9595
Fax: 520 621 1259
            High quality sequence stop: 627.
Location/Qualifiers
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OMAP Project
                                                                                                                                                                                                                                                                              Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DN
/db_xref="taxon:4533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="OB_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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/lab_host="DH10B"
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/tlssue_type="leaves"
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Pred. No. 53;
O; Mismatches
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ne IMAGE:6426298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D.,

R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                              CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 393)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                    Insert Length: 488 Std Error: 0.00 Seq primer: -40UP from Gibco.
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/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 101"
/clone_lib="NIH_MGC 101"
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
/note="Organ: pote_1: 
/organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                             Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 56;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.S. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco
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Unpublished (1997)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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EST.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
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1 (bases 1 to 481)
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/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP GC4 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
/lab_host="DH10B"
/clone lib="WCI_CGAP_Pan1"
/clone lib="WCI_CGAP_Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sal1;
/note="Organ: Cloned unidirectionally. Primer: Oligo dT.
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
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/lab_host="DH108"
                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                       /clone="IMAGE:2877161"
/tissue_type="adenocarcinoma"
                                                                                                                                                                                                /mo1_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 CCCCCAACGTTGCACACTCACTGCCTTTGCAGGGTTGGGGCTTCCAGTCACAGGGTCCC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69;
                                                                                                         69;
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1 (bases 1 to 523)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI818367.1 GI:5437446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGCCCATGCTGANTTCCTGCCCCTGGAGGGAAGGGGCCGAGGGGCTTCCCGTCCC
                         ATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAACCAAGGGAGG
                                                   CCGCCCATGCTGGCTCAGTTCCTGCCCCTGGAGGGAAGGGGCCGAGGGGCTTCCTGTCCC
                                                                              CCCCCAACGTTGCACACTCACTGCCTTTGCAGGGTTGGGGCTTCCAGTCACAGGGTCCC
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                                                                                                                                                                                      /clone_lib="NCI_CGAP_Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: OIigo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
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/tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                     6.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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Pred. No. 6
                                                                                                                     Score 37.8;
Pred. No. 65;
                                                                                                         Mismatches
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sapiens cDNA clone IMAGE:2419743
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                                                                                                                                  Length 523;
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ACCESSION
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Best Local Similarity
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Tel: 402 762 4396
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_ait option. Vector identified with
cross_match v0.990329.
Plate: TMW8015 row: K column: 23
Seq primer: TAGAAGGCACAGTCGAGG.
Locarion/Qualifiers
1 592
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R991143 MARC 4PIG Sus scrofa cDI

CF795053

CF795053.1 GI:37799626

EST.

Sus scrofa (pig)
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AA983291
AA983291.1
EST.
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oq56e01.s1 NCI_CGAP_Kid5
mRNA_sequence.
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Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W. Porcine EST collection using a normalized library constructed from embryos representing early developmental stages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                               CCGTCCAGGGCTCGGCGTCTCTCCACCTTCTGCGTCCTGTGCACCAGGGCTCAGC 55
                                                                                                                                                                                                TGGTCCCCAGCACTGCCCGCCGCCTCTGCGATGCAGTCCTCCTGGCCACCTGAGAACAGC 532
                                                                                                                                                                                                                                                                GAGGGTGGGGCTGGGCCAAGGCCCACCAGGTCTGAGTCAGAGCCAGAGGCAGGAAGC 472
                                                                                                                                                                                                                                                                                                                         TCATGAAACCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGA 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DA, ARS, US Meat Animal Research Center
Box 166, Clay Center, NE 68933-0166, USA
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                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sus scrofa"
/mol type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: Not Library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."
                 GI:3161816
                                                                                                                                                                                                                                                                                                                                                                                    6.7%;
50.6%;
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                                                                                                                                                                                                                                                                                                                                                                                    Score 37.6;
Pred. No. 75;
                                                                Homo
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                                                          294 bp mRN
Homo sapiens
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cDNA 3', mRNA
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                                                                                 mRNA
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                                                              NA linear EST 23-JUL-1998 CDNA clone IMAGE:1590360 3',
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RESULT 15
BG230743
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                  159
                                                                                                                                                                                                                                          279
                                                                                                                                                                                                                                                                        371 CT 372
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                                                                                                                                                                                                                                                                                                                                                                                                  251 CCCCCAACGTTGCACACTCACTGCCTTTGCAGGGTTGGGGCTTCCAGTCACAGGGTCCC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                  69;
                                                                                                                                        naf39e01.x1 Soares_NPBMC Homo
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
                                                                                                              mRNA sequence.
BG230743
                                                                                                                                                             BG230743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih
Tissue Procurement: Chri
Emmert-Buck, M.D., Ph.D.
                                               Homo sapiens
                                                                                               BG230743.1 GI:12725789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 294)
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                      CCGCCCATGCTGGCTCAGTTCCTGCCCCCTGGAGGGGAAGGGGGCCCGAGGGGCTTCCCGTCCC
                                                                                                                                                                                                                                          ე:
                                                              sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1590360"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37.2; D
Pred. No. 84;
0; Mismatches
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                                                                                                                                                          360 bp
                                                                                                                                           sapiens cDNA clone IMAGE:4143433
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                               53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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JOURNAL COMMENT
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AUTHORS
Search completed: March 25, 2006, 18:16:21 Job time: 3248 secs
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Best Local Similarity
Matches 69; Conserv
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                                                                273
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                                                                                                                                                                                          153 CCGCCCATGCTGGCTCAGTTCCTGCCCCTGGAGGGAAGGGGCCGAGGGGCTTCCCGTCCC 212
                                                                                                                                                                                                                           251
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

cDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

info@dimage.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D. and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 360)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 338.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -40UP from Gibco
                                                                                        CT 372
                                                                3:
                                                                                                                                ATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCTCGCAGTCATGAAACCAAGGGAGG 370
                                                                                                                                                                                                               CCCCCAACGTTGCACACTCACTGCCTTTGCAGGGTTGGGGGCTTCCAGTCACAGGGTCCC 310
                                                                  274
                                                                                                                                                                                                                                                         6.6%;
ilarity 56.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:4143433"
/tissue_type="lymphocyte"
/tissue_type="lymphocyte"
/lab_host="H10B (phage=resistant)"
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
seq length: 2000000000
                                                                                                        Issued_Patents NA:*

1: /cgm2 6/ptodata/1

2: /cgm2 6/ptodata/1

3: /cgm2 6/ptodata/1

4: /cgm2 6/ptodata/1

5: /cgm2 6/ptodata/1

5: /cgm2 6/ptodata/1

6: /cgm2 6/ptodata/1

7: /cgm2 6/ptodata/1

8: /cgm2 6/ptodata/1

9: /cgm2 6/ptodata/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC
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                                                                                                  /cgn2_6/ptodata/1/ina/1_COMB.seq:*
/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/P_COMB.seq:*
/cgn2_6/ptodata/1/ina/P_COMB.seq:*
/cgn2_6/ptodata/1/ina/B_COMB.seq:*
/cgn2_6/ptodata/1/ina/Backfiles1.seq:*
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Biocceleration Ltd.
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## SUMMARIES

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702	35457	23902	1734	1734	601	199945	77536	77536	2508	108441	108440	601	239527	6872	435	11276	42610	1338	4050	954	474	19319	23856	Length	
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US-08-136-277-20	US-09-949-016-15472	US-09-949-016-14220	US-09-182-145-18	-09-182	US-09-949-016-88252	US-09-949-016-15436	US-09-940-316B-1	US-09-410-551B-1	US-10-104-047-1958	US-09-949-016-14090	US-09-949-016-12065	US-09-949-016-94858	-09	US-09-949-016-15483	US-09-621-976-17564	US-09-949-016-14499	US-09-949-016-13882	US-09-843-905A-11	US-09-902-540-604	US-09-902-540-6966	US-09-621-976-18033	US-09-949-016-14107	US-09-949-016-15732	ID	
Sequence 20,		Sequence 14	Sequence 18	Sequence 17														Sequence 11,				Sequence 14	Sequence 15	Description	
Appl	15472, A	14220, A	•	, Appl	88252, A	436, A	<ol> <li>Appli</li> </ol>	Appli	1958, Ap	14090, A	12065, A	•	15980, A	•	-	14499, A		, Appl	604, App	6966, Ap	18033, A	14107, A	732, A	:	

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32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4			32.6		32.6		32.6			
5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.8	5. 8	5. 8	s. 8	ა დ	5. 8	5.8	ۍ 8	5.8
28958	20513	17557	8260	2277	2233	601	601	601	601	364	51671	51671	13821	6202	6201	1335	1332	1089	702
N	w	ω	w	w	w	w	w	w	w	w	w	w	w	ω	w	ω	w	w	w
US-08-258-261B-6	US-09-949-016-13930	US-09-949-002-848	US-09-949-016-14285	US-09-495-050A-155	US-09-484-970B-141	US-09-949-002-10196	US-09-949-002-6132	US-09-949-016-194766	US-09-949-016-91825	US-09-621-976-17202	US-09-949-016-15962	US-09-949-016-12068	US-09-949-016-13690	US-09-949-016-16322	US-09-949-016-12048	US-09-252-991A-9690	US-09-252-991A-9561	US-09-252-991A-9606	US-08-835-734-20
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
6, Appli	13930, A	848, App	14285, A	155, App	141, App	10196, A	6132, Ap	194766,	91825, A	17202, A	15962, A	12068, A	13690, A	16322, A	12048, A	9690, Ap	9561, Ap	9606, Ap	20, Appl

## ALIGNMENTS

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FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15732

LENGTH: 23856

TYPE: DNA

ORGANISM: Human

FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(23856)

OTHER INFORMATION: n = A,T,C or G

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US-09-949-016-15732/c
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                                                                                                                                                                                                                                                                                                                                               Query Match 6.8%;
Best Local Similarity 48.8%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15732, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                       17528
                                                                                                                                                                                                                                                         17648 TCCGGCCCCAGAGGTGGCCCACGTCTGGGGGGTCACTGCGGCAGGCCAAGGCCTGGGGG 17589
                                                                                                                                                                  17588 CCÁCCGGAGCCCCACCCTGCGTGGTCCCACCCGGAGCATCGCTTGGGCCCCGGCACTCAC 17529
                                                                                                                     199
                                                                                                                                                                                                      139 GCACAGGGGCTCCATACAGCTTACTCAGTGACAATCGAGTCCCTGGTGCCAGCCTCTGGA 198
259 CGTTGCACACTCACTGCCTTTGCAGGGTTGG 289
                                                                                                                                                                                                                                                                                                 79 TCCTGAGGCAGGCCAGGGCAGCCGTCAGGTGGGTGACGGCAGGGGTCTTGCCATGGTGG 138
                                                                          AGTGAGCAGGAGGCACTTGTTCTCCTTGATGGCACCCAGGCAGCCCACGAAGCCGATGGC 17469
                                                                                                                Score 38.2; DB 3; Length 2
Pred. No. 1.4;
0; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Length 23856;
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17468

CATGACAAAGGCGCCGGTGATGATGAGCAGG 17438

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APPLICANT: Dumás Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
FILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 18033
LENGTH: 474
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-09-621-976-18033
; Sequence 18033, Application US/09621976
; Patent No. 6639063
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US-09-949-016-14107
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                                                                            ; LOCATION: 16; OTHER INFORMATION: n=a, US-09-621-976-18033
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Best Local S
Matches 69
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 14107
LENGTH: 19319
TYPE: DNA
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                   Matches
                               Query Match
Best Local Similarity
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                       ORGANISM: Homo sapiens FEATURE: nisc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCCAACGTTGCACACTCACTGCCTTTGCAGGGTTGGGGCTTCCAGTCACAGGGTCCC
                 Conservative
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                6.3%; Score 35.4; DB 3;
13.7%; Pred. No. 2.4;
ative 147; Mismatches 174;
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Pred. No. 2.5;
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                                               Length 474;
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RESULT 5
US-09-902-540-604
; Sequence 604, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6966
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US-09-902-540-6966/c
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CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 6966
LENGTH: 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                               6.2%;
Local Similarity 53.7%;
hes 73; Conservation
344
                                                                                               404
                                                                                                                                            467
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                                                                                                                                                                                                                                         407 TAGTGAGAGGGTTGGGCTGGGCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGCA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 WAAAARGGWTWA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 CYKGACYYMWKRWYCSSCCMMYTKGGGSMWTTTWMMRRRKKSYKRWTKGKKKKKTTWMMA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
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                                                                                                                           GEAAGCTGGTCCCCAGCACTGCCCGCCGCCTCTGGGATGCAGTCCTCCTGGCCACCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYYTTYYKRMCCYYMRKTTYCMMWYSRWWRGSMWTARGAMWMCYWWYYYMAARKKKXMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGCCGTCAGGTGACGGCAGGGGTCTTGCCATGGTGGGCACAGGGGCTGCATACA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCCYKSCYYSGNCYYCCMARKWRSYKGGRMYKSMRGSSSCYKSCMMCMMSKYCSGSYKK 63
                                               AACAGCCTGTAGAGAG 542
                                                                                               CGGCTCCCCTTGACGGGAATCCATACCCGGACGGCCATGCAGTCCCCCTGGGCTTCTTCG
                                                                                                                                                                                            TCGTGCGCGTGCCGCGCTTCGAGGAGCCCCCACGAGCACGTCCTTGGCCGCGTCCGTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCTTTGATTTA 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTTACTCAGTGACAATCGAGTCCCTGGTGCCAGCCTCTGGAAGTCTGGAAGTGAGCAAT
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AGCTGCCAGTAGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAAGGTCCCTCGCAGTCATGAAACCAAGGGAGGCTTGGGAAACCACATCTGAAGGGCAT 396
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                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                      Score 35.2; DB Pred. No. 3.4; 0; Mismatches
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                                                                                                                                                                                                                                                                                           63;
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                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 1338
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Best Local
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SEQ ID NO 604
LENGTH: 4050
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bird, Timothy A.
APPLICANT: Cosman, David J.
TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES
FILE REFERENCE: 2990-A
CURRENT APPLICATION NUMBER: US/09/843,905A
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/200,198
PRIOR FILING DATE: 2000-04-28
NUMBER OF SECTION NUMBER: US 60/200,198
PRIOR FILING DATE: 2000-04-28
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APPLICANT:
APPLICANT:
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APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: MYXOCOCCUB xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc feature
LOCATION: (513)...(513)
OTHER INFORMATION: unsure
                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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LOCATION: (1)..(4050)
OTHER INFORMATION: unsure at all n locations
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                                                         AGGACGGCTCTCATCGACCTGTGTGGGGGCCACACTGCTGTGGCGCACACCGGCGGGGC
                                                                                           AGGGAGGCTTGGGAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTGGGGC 423
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Gregory J.
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53.7%;
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Pred. No. 4.3;
0; Mismatches
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Pred. No. 5.5;
0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOSTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 13882
LENGTH: 42610
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; ORGANISM: Human
US-09-949-016-13882
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Sequence 14499, Application US/09949016 Patent No. 6812339
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Matches 110; Conserva
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Best Local
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: CL001307
                                                                                                                              13769
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                                                                                                                                                                                                                                                   373
                                                                                                                                                                                                                                                                                                                 313 CCACGTACCAGGCCCAGGTGGCAGAAGGTCCCTCGCAGTCATGAAACCAAGGGAGGCT 372
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                                                                                                                                                                  CAAGGCCACCAGGTCTGAGTCAGAGCCAGGAGGCAGGAAGCTGGTCCCCAGCACTG 487
                                                                                                                                                                                                         GGGGCAGGGTGGGGTGAGGCCCCAAGGAAACCCATGTGGACTGAAGGGGAGGGGAGGGGAGGGCAG
                                                                                                                                                                                                                                                                                            TCACCAAGCGGTAGCACTCTGACCAGTGGGCCTGGGTCCTATGACAGCTCCTGTGGCT
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                                                                                                                              CACTCCCAGAGGGGTGGACGCAGGACCAGCCGGTGGGGATGGTGGGGGCAGCTCTG
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307

AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498

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APPLICANT: Giordano, J.Y.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human P
FILLE AFEBERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 17564

LENGTH: 435

TYPE: DNA

ORGANISM: Homo sapiens
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              Sequence 15483, Application Patent No. 6812339 GENERAL INFORMATION:
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GENERAL INFORMATION:
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LENGTH: 11276
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Best Local Similarity
Matches 77; Conserv
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Best Local S
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ORGANISM: Human
FEATURE:
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version
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 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(11276)
OTHER INFORMATION: n = A,T,C or
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VENTER, J. Craig et al.
                                                                                                                             CTCCATCCCCTAATCCTGTGTCACCTGTG 314
                                                                                                                                                          CGCAGTCATGAAACCAAGGGAGGCTTGGG 376
                                                                                                                                                                                           GGAGCGCCGAGGCAGTGACTGCGACGCAAACATCAAACCAGATGCAAACAGATTCATTAT
                                                                                                                                                                                                                         GGGGCTTCCAGTCACAGGGTCCCATCCACGTACCAGCCCAGGTGGCTGCAGAAGGTCCCT 347
                                                                                                                                                                                                                                                        AGGAAGTTGTCGCCGCGGCCATTTCCCCCCAGTGCCGCAACTTGCTGGCCTTGGAGGGGGA
                                                                                                                                                                                                                                                                                      AGGAACAGCATCTGGAGACCTGACCACCCCTCCT 7557
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                                               US/09949016
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Pred. No.
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Pred. No. 6.6;
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17;
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                                                                                                                                                                                                                                                                                                                                                    Length 435;
                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                     Gaps
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOSTWARE: FASESEQ FOR WINDOWS Version 4.0
SEQ ID NO 15980
LENGTH: 239527
TYPE: DWA
ORGANISM: Human
FEATURE:
LENGTH: 239527
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                                                                 US-09-949-016-15980
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
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SEQ ID NO 15483
LENCTH: 6872
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                              NAME/KEY: misc_feature
LOCATION: (1)...(239527)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (1)...(6872)
OTHER INFORMATION: n =
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Match 6.0%;
Local Similarity 48.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 6.0%; Local Similarity 54.4%;
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Score 33.8;
Pred. No. 52;
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Pred. No. 16;
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                      Length 239527;
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Matches

Conservative

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Mismatches

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US-09-949-016-12065
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US-09-949-016-94858
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/331,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEO TO NOTE: 2000-09-08
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Sequence 12065, Application US/09949016
Patent NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAGTGAGAGGGTGGGGCTGGGCCAAGGCCACCAGGTCTGAGTCAGAGCCAGAGGC 465
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                                                                                                                                                                                                                                                                                                                       AGGAACAGCATCTGGAGACCTGACCACCCCTCYT 302
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ilarity 50.6%;
Conservative
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RESULT 15

US-10-104-047-1958

Sequence 1958, Application US/10104047 Patent No. 6943241

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. 6943241el full length
FILE REFERENCE: H1-A0105
CURRENT BEPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:

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                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14090
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                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
RUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14090
LENGTH: 108441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12065
LENGTH: 100440
                                                                                                                                                             Query Match
Best Local S
                                                                                                                                              Matches
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20
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ORGANISM: Human
                                                                                                                                                           Local
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81586 GCTGTCTTGGGGTACACTGGGACTGGAAGGAGCTGCCTTCCTGA 81629
                                                                      81526
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                                  126 CTTGCCATGGTGGGCACAGGGGCTGCATACAGCTTACTCAGTGA 169
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o. 6812339
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                                                                                                          66 AGGCGAGGGAGCCTCCTGAGGCCAGGGCCAGGCCGTCAGGTGGCTGACGGCAGGGGT 125
                                                                                                                                      6.0%;
l Similarity 57.7%;
60; Conservativo
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Similarity 57.7%;
                                                                      AGGTGGTGAAACCACTATGGGCCTGGCCAAATCAGCAAGAAGGGGGCTGGAGGAAGGGCA 81585
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                                                                                                                                          ; Score 33.6; D; ; Pred. No. 46; 0; Mismatches
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Pred. No. 46;
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Result
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Maximum DB
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                                                                                                                                       /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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US-10-027-632-142126
US-10-108-260A-578
US-10-113-155-10
US-10-146-731-10
US-10-141-761-10
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70. A	Sequence 258, App	Sequence 258, App	Sequence 3312, Ap	Sequence 1312, Ap	Sequence 10143, A	Sequence 1312, Ap	Sequence 258790,	Sequence 258790,	Sequence 11, Appl		Sequence 11, Appl	Sequence 52013, A	Sequence 17803, A	Sequence 5702, Ap	Sequence 60160, A	Sequence 20932, A	Sequence 1, Appli	Sequence 492, App	Sequence 57042, A	Sequence 12287, A	Sequence 1311, Ap

ALIGNMENTS

## ; SOFTWARE: FastSEQ for Windows ; SEQ ID NO 142127 ; LENGTH: 700 ; TYPE: DNA ; ORGANISM: Human US-10-027-632-142127 RESULT 1 US-10-027-632-142127 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR FILING DATE: 2000-04-20 PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29 PRIOR FILING DATE: 2000-02-29 PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23 PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-08-09 PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09 PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09 PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09 PRIOR APPLICATION NUMBER: US 60/146,002 Best Loc Matches GENERAL INFORMATION: APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome Sequence 142127, Application US/10027632 Publication No. US20020198371A1 Query Match Best Local S CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12 FILE REFERENCE: 108827.129 CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 563; ۲ Similarity GCAGCCCTGCCTCAGAAAACAGAAGGACGCAGCACACTCACGGTGACTCACCCCCCATGTG Conservative 100.0%; Score 564; DB 5; 99.8%; Pred. No. 2.8e-165; tive 1; Mismatches 0; Version 4.0 Length 700; Indels 0 Gaps

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121 GGGGTCTTGCCATGGTGGGCACAGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCC 180

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FILE REFERENCE: 108827.129
FILE REFERENT HORDER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR REPLICATION NUMBER: US 60/198,676
PRIOR REPLICATION NUMBER: US 60/193,483
PRIOR RILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR REPLICATION NUMBER: US 60/187,363
PRIOR FILING DATE: 1999-11-23
PRIOR REPLICATION NUMBER: US 60/156,358
PRIOR RILING DATE: 1999-09-28
PRIOR REPLICATION NUMBER: US 60/146,002
PRIOR PRILING DATE: 1999-08-09
SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 142127
LENGTH: 700
TYPE: DNA
ORGANISM: Human
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                                                               Query Match
Best Local Similarity
Matches 563; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                               Sequence 1, Application US/10798652

Publication No. US20040219582A1

GENERAL INFORMATION:
APPLICANT: Yongjun Guo
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISM IN
TITLE OF INVENTION: FGF-3 GENE AND METHODS OF USE THE
FILE REFERENCE: 3382-PO3136US01

CURRENT APPLICATION NUMBER: US/10/798,652

CURRENT FILING DATE: 2004-03-11

PRIOR APPLICATION NUMBER: 60/455,698

PRIOR FILING DATE: 2003-03-17

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FASCESQ for Windows Version 3.0

SEQ ID NO 1

LENGTU. 564
                                                                                                                                                                    ; LENGTH: 564
; TYPE: DNA
; ORGANISM: Homo sapien
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: n is cytosine or thymine
US-10-798-652-1
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US-10-798-652-1
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                                                                                                             Query Match
Best Local Similarity
Matches 563; Conserv
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AGCACTGCCCGCCGCCTCTGCGATGCAGTCCTCCTGGCCACCTGAGAACAGCCTGTAGAG
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                                                                                                               Conservative
                                                                                                                           99.8%;
                                                                                                             0;
                                                                                                             Score 563; DB 8;
Pred. No. 4.2e-165;
0; Mismatches 1;
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                                                                                                                                      Length 564
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SEQUENCE 642, Application US/1032281

PUBLICATION NO. US20040126762A1

GENERAL INFORMATION:
APPLICANT: David W. MOXI'S
APPLICANT: MARC S. Malandro
ITILE OF INVENTION: NOVEL Compositions and Mel-
FILE REFERENCE: 529452001000

CURRENT APPLICATION NUMBER: US/10/322,281

CURRENT FILING DATE: 2002-12-17

NUMBER OF SEQ ID NOS: 866

SOFTWARE: FMSACSEQ for Windows Version 4.0

SEQ ID NO 642
LENGTH: 29340
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; ORGANISM: Homo
US-10-322-281-642
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Best Local
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Local Similarity 99.8%;
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                       CTGGTGCCAGCCTCTGGAAGTCTGGAAGTGAGCAATGTTTCCCATTAAGGAAAGTGTGTG
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                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                    Score 553; DB 7;
Pred. No. 9.9e-162;
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FILE REPERENCE: 108827.129
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1090-12-3
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-08-09
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US-10-027-632-142126
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                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 142126, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Polymorphisms
FILE REFERENCE: 108827.129
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                                                                                                                                                                        Similarity
                         GGGGTCTTGCCATGGTGGGCACAGGGGCTGCATACAGCTTACTCAGTGACAATCGAGTCC
                                                                                   CCAAGGGAGGCTTGGGAAAACCACATCTGAAGGGCATGGCTTTGATTTAGTGAGAGGGTTG
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                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                  98.0%;
                                                                                                                                                                                                                                                             Score 552.6; DB 5;
Pred. No. 7.9e-162;
1; Mismatches 0;
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-04-20
PRIOR RELING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR PELLING DATE: 1909-11-23
PRIOR PELLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 142126
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                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-142126
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US-10-027-632-142126
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                                                                                                                                     Query Match
Best Local Similarity
Matches 563; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                 ENGTH: 855
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                                                                                GCAGCCCTGCCTCAGAAAACAGAAGGACGCAGCACACTCACGGTGACTCACCCCCCATGTG
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GCAGCCCTGCCTCAGAAAACAGAAGGACGCAGCACACTCACGGTGACTCACCCCCATGTG
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                                                                                                                                         Conservative
                                                                                                                                                            98.0%;
                                                                                                                                     Score 552.6; DB 6;
Pred. No. 7.9e-162;
1; Mismatches 0;
                                                                                                                                         Indels
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APPLICANT: Mang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Gen.
FILE REFERENCE: 108827.135
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR PRIOR PRIOR DATE: 2001-05-09
NUMBER OF EGG ID NOS: 957086
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 734471
LENGTH: 541
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                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-734471
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US-09-925-065A-734471
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                                                                                                                       Query Match
Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 734471, Application US/09925065A Publication No. US20050228172A9
                                                                                                          Local 59;
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Similarity 64.8%;
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                                         GCCCTCCCTCGGAAACCAGGAAGGCTGGGCACCCTCCGTGGGCCTCACCCTCATTTGGAA 501
                                                                                  GCCCTGCCTCAGAAAACAGAAGGACGCAGCACACTCACGGTGACTCACCCCCATGTGGCT 63
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  GGAGGCGAGGGAGCCTCCTGAGGCAGGGCCA 94
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                                                                                                                         Conservative
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                                                                                                                       Score 39.8; DB 4;
Pred. No. 0.056;
0; Mismatches 32;
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US-10-123-155-10
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US-10-108-260A-578/c
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C30
CURRENT APPLICATION NUMBER: US/10/123,155
CURRENT FILING DATE: 2002-04-15
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 578, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/10123155 Publication No. US20030068794A1
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SEQ ID NO 578
LENGTH: 2777
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                                                                                                                                               Tumas, Daniel
Watanabe, Colin K
Wood, William
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Stewart, Timothy A.
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                                                                                                                                                                                                                                                                                                                           Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                           Filvaroff, Ellen
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Pred. No. 0.22;
0; Mismatches 1
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APPLICANT: APPLICANT: APPLICANT:

Watanabe, Colin K Wood, William Tumas, Daniel APPLICANT: APPLICANT:

Stewart, Timothy A. Smith, Victoria Sherwood, Steven Godowski, Paul Goddard, Audrey

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C323
CURRENT APPLICATION NUMBER: US/10/146,731
CURRENT FILING DATE: 2002-05-15

APPLICANT: APPLICANT: APPLICANT:

APPLICANT: APPLICANT:

Gerritsen, Mary E Gao, Wei-Qiang Filvaroff, Ellen

APPLICANT:

Gurney, Austin L

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US-10-123-155-10
                                                             GENERAL INFORMATION
                                                                        Sequence 10, Application US/10146731 Publication No. US20030129692A1
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Best Local
 APPLICANT:
APPLICANT:
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                              APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maur
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                                                                                                                                                                      PAREKLT 542
                                                                                                                                                                                                   ATGCAGT 509
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DeForge, Laura
Desnoyers, Luc
                               Beresini, Maureen
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; Prior Application removed -
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 10
; LENGTH: 594
; TYPE: PRT
; ORGANIAN: Homo Sapien
US-10-146-731-10
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US-10-140-472-10
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T: Zhang, Zemin
INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
INVENTION: ACIDS ENCODING THE SAME
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Gao,Wei-Qiang
Gerritsen,Mary E.
Goddard,Audrey
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                                                                                                                                                                                                                                                                                                    Application US/10140472
No. US20030138888A1
                                                                                                                                     Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                            DeForge, Laura
Desnoyers, Luc
                                                               Watanabe, Colin K
                                                                         Tumas, Daniel
                                                                                                                      Sherwood, Steven
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                                                                                                          Smith, Victoria
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CURRENT APPLICATION UNMER: US/10/140,472
CURRENT FILING DATE: 2002-05-06
Prior Apploication removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
SEQ ID NO 10
LENGTH: 594
TYPE: PRT
ORGANISM: Homo Sapien
S-10-140-472-10
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Matches
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PAREKLT
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Sequence 10, Application US/10141761
Publication No. US20030148432A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen RESULT 12 US-10-141-761-10 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Goddard, Audrey Godowski, Paul J. Gurney, Austin L. Watanabe, Colin K Wood, William Tumas, Daniel Stewart, Timothy A. Smith, Victoria Sherwood, Steven Gerritsen, Mary E. Gao, Wei-Qiang

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RESULT 13
US-10-142-885-10
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APPLICANT: Beresini, Mauree
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
                                                                                                                                                                                                                 Sequence 10, Application US/10142885 Publication No. US20030157604A1
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              APPLICANT:
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CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or F
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 10
                                             APPLICANT:
                                                             APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333OR1C198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo
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                                        Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Stewart,
            Sherwood, Steven Smith, Victoria
                                                                                                                       Filvaroff, Ellen
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Pred. No. 0.24;
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RESULT 14 US-10-158-790-10

Sequence 10, Application US/10158790 Publication No. US20030180879A1 GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: Baker Kevin P
APPLICANT: Beresini, Mau
APPLICANT: DeForge, Laux
APPLICANT: Desnoyers, Lu
APPLICANT: Filvaroff, El
APPLICANT: Gao, Wei Qian
APPLICANT: Gerritsen, Ma

Beresini, Maureen DeForge, Laura

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Gao, Wei-Qiang Gerritsen, Mary E. Desnoyers, Luc Filvaroff, Ellen

APPLICANT: APPLICANT: APPLICANT:

Goddard, Audrey Godowski, Paul

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; LENGTH: 594
; TYPE: PRT
; ORGANISM: Homo S
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Best Local Similarity 7.0%;
Matches 34; Conservative 17
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APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C248
CURRENT APPLICATION NUMBER: US/10/142,885
CURRENT FILING DATE: 2002-05-10
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                                ATGCAGT
                                                                GDRYRRGGRGLRHHSSSRSRSSWSLSPSRSRSLTRSRSHSPSPSQSRSRSRSRSQSPSPS
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542
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%; Pred. No. 0.24;
176; Mismatches 277;
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RESULT 15
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-158-790-10
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                                                Sequence 10, Application US/10137871
Publication No. US20030207350A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Desroyers, Luc
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 10
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CURRENT APPLICATION NUMBER: US/10/158,790

CURRENT FILING DATE: 2002-05-30
                 APPLICANT:
     APPLICANT
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Beresini, Maureen
DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Search completed: March 25, Job time : 682.5 secs

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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 10
LENGTH: 594
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CURRENT APPLICATION NUMBER: US/10/137,871
CURRENT FILING DATE: 2002-05-03
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                    ATGCAGT 509
                                                                      GDRYRRGGRGLRHHSSSRSRSSWSLSPSRSRSLTRSRSHSPSPSQSRSRSRSRSQSPSPS
                                                                                                          AGGTCTGAGTCAGAGCCAGAGGCAGGAAGCTGGTCCCCAGCACTGCCCGCCGCCTCTGCG
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Watanabe, Colin K
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7.0%; Pred. No. 0.24;
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